GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 26, 2005, 15:28:42 ; Search time 133.689 Seconds
(without alignments)
659.602 Million cell updates/sec

Title: US-09-545-998B-2
Perfect score: 1301
Sequence: 1 MGAWAMLYGVSMLCVLDLGQ.....PEEERGEQTEEKCHLGGRWP 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1301	100.0	228	2	AAW37838	Aaw37838 Amino aci
2	1301	100.0	228	2	AAW49016	Aaw49016 Mouse glu
3	1301	100.0	228	6	ADA09440	Ada09440 Murine GI
4	1301	100.0	228	8	ADH43110	Adh43110 Mouse glu
5	1079	82.9	222	2	AAW49018	Aaw49018 Mouse glu
6	1079	82.9	294	2	AAW49017	Aaw49017 Mouse glu
7	735.5	56.5	240	8	ADR46662	Adr46662 Cancer-as
8	735.5	56.5	241	2	AAW37839	Aaw37839 Amino aci
9	735.5	56.5	241	2	AAY06605	Aay06605 Human TNF
10	735.5	56.5	241	3	AAB33431	Aab33431 Human PRO
11	735.5	56.5	241	3	AAY71467	Aay71467 Human PRO
12	735.5	56.5	241	3	AAB27651	Aab27651 Human pro
13	735.5	56.5	241	3	AAY95895	Aay95895 Human tum
14	735.5	56.5	241	3	AAB24409	Aab24409 Human PRO
15	735.5	56.5	241	4	AAB47054	Aab47054 Human PRO
16	735.5	56.5	241	4	AAB20115	Aab20115 Human imm
17	735.5	56.5	241	4	AAB53090	Aab53090 Human ang
18	735.5	56.5	241	4	AAB47289	Aab47289 PRO364 po
19	735.5	56.5	241	4	AAB50982	Aab50982 Human PRO
20	735.5	56.5	241	4	AAB50910	Aab50910 Human PRO
21	735.5	56.5	241	5	AAE28161	Aae28161 Human TR1
22	735.5	56.5	241	6	ABU08442	Abu08442 Amino aci
23	735.5	56.5	241	6	AAO16574	Aao16574 Human tum
24	735.5	56.5	241	6	AAO23091	Aao23091 Human ene
25	735.5	56.5	241	7	ADN39966	Adn39966 Cancer/an
26	735.5	56.5	241	8	ADH43131	Adh43131 Human TNF
27	735.5	56.5	241	8	ADL91869	Adl91869 Human PRO
28	735.5	56.5	241	8	ADO20289	Ado20289 Human PRO
29	735.5	56.5	241	8	ADP55559	Adp55559 Human PRO
30	735.5	56.5	241	8	ADT94287	Adt94287 Human PRO
31	734.5	56.5	235	3	AAY44825	Aay44825 Human mol
32	734.5	56.5	235	6	AAO16576	Aao16576 Human tum
33	734.5	56.5	235	6	AAO23093	Aao23093 Human ene
34	703	54.0	228	2	AAW37840	Aaw37840 Truncated
35	703	54.0	228	6	AAO16577	Aao16577 Human tum
36	703	54.0	228	6	AAO23099	Aao23099 Human ene
37	703	54.0	234	3	AAY95879	Aay95879 Human tum
38	703	54.0	234	3	AAY52158	Aay52158 Tumour ne
39	703	54.0	234	5	AAE28158	Aae28158 Human TR1
40	703	54.0	234	6	ABU08439	Abu08439 Amino aci
41	703	54.0	234	6	AAO16575	Aao16575 Human tum
42	703	54.0	234	6	ADA09435	Ada09435 Human TR1
43	703	54.0	234	6	AAO23092	Aao23092 Human ene
44	703	54.0	234	8	ADH43105	Adh43105 Human TNF
45	703	54.0	234	8	ADO20305	Ado20305 Human PRO

ALIGNMENTS

RESULT 1
AAW37838
ID AAW37838 standard; protein; 228 AA.
XX
AC AAW37838;
XX
DT 28-JUL-1998 (first entry)
XX
DE Amino acid sequence of the mouse 312C2 T cell protein.
XX
KW Mouse 312C2 T cell protein; thymus cell; spleen cell; T cell;
KW antigen-specific T cell proliferation; cytokine production by T-cell;
KW apoptosis; cancer; haematopoietic cells; lymphoid cell;
KW autoimmune disorders.
XX
OS Mus sp.
XX
PN WO9806842-A1.
XX
PD 19-FEB-1998.
XX
PF 14-AUG-1997; 97WO-US013931.
XX
PR 16-AUG-1996; 96US-00689943.
PR 07-OCT-1996; 96US-0027901P.
XX
PA (SCHE) SCHERING CORP.
XX
PI Gorman DM, Randall TD, Zlotnik A;
XX
DR WPI; 1998-159534/14.
DR N-PSDB; AAV19152.
XX
PT Isolated 312C2 T cell gene - used to develop products for treating, e.g.
PT cancers, auto-immune disorders, transplantation rejection and other T
PT cell disorders.
XX
PS Claim 2; Page 57-58; 71pp; English.
XX
CC This is the amino acid sequence of the mouse 312C2 T cell protein. The
CC 312C2 proteins are expressed in thymus cells and are induced on T cells
CC and spleen cells following activation. Engagement of 312C2 stimulates
CC proliferation of T cell clones, antigen-specific proliferation and
CC cytokine production by T-cells, and potentiates T cell expansion or
CC apoptosis. The products can be used in the treatment of conditions
CC associated with abnormal physiology or development, including abnormal
CC proliferation, e.g. cancerous conditions or degenerative conditions. They
CC can be used in the regulation or development of haematopoietic cells,

```
CC   e.g. lymphoid cells which affect immunological responses, e.g. autoimmune
CC   disorders
XX
SQ   Sequence 228 AA;

  Query Match             100.0%;  Score 1301;  DB 2;  Length 228;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-112;
  Matches  228;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60

Qy         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120

Qy        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180

Qy        181 RRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP 228
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP 228


RESULT 2
AAW49016
ID   AAW49016 standard; protein; 228 AA.
XX
AC   AAW49016;
XX
DT   29-SEP-1998  (first entry)
XX
DE   Mouse glucocorticoid induced TNFR-family related protein (GITR).
XX
KW   Mouse glucocorticoid induced TNFR-family related protein; lymphocyte;
KW   GITR; tumour necrosis factor; apoptosis; hodgkin's disease; GITR-B;
KW   GITR-C.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .19
FT                   /note= "Signal peptide"
FT   Region          29. .60
FT                   /note= "Cysteine pseudorepeat"
FT   Modified-site   36
FT                   /note= "N-glycosylated"
FT   Modified-site   40
FT                   /note= "N-glycosylated"
FT   Region          62. .100
FT                   /note= "Cysteine pseudorepeat"
FT   Region          103. .141
FT                   /note= "Cysteine pseudorepeat"
FT   Modified-site   121
FT                   /note= "N-glycosylated"
FT   Modified-site   134
FT                   /note= "N-glycosylated"
FT   Region          154. .176
FT                   /note= "Probable transmembrane domain"
FT   Modified-site   199
FT                   /note= "Possibly phosphorylated"
XX
PN   WO9824895-A1.
XX
PD   11-JUN-1998.
XX
PF   08-NOV-1997;   97WO-EP006252.
XX
PR   02-DEC-1996;   96GB-00025074.
XX
PA   (PHAA ) PHARMACIA & UPJOHN SPA.
XX
PI   Riccardi C;
XX
DR   WPI; 1998-333315/29.
DR   N-PSDB; AAV32773.
XX
PT   New isolated glucocorticoid induced TNFR related polypeptide - used to
PT   stimulate lymphocyte activity and cell death rescue, useful to, e.g.
PT   develop products to suppress lymphocyte activity and induce apoptosis.
XX
PS   Claim 13; Page 36-37; 53pp; English.
XX
CC   The present claimed sequence represents a mouse glucocorticoid induced
CC   TNFR-family related protein (GITR). The invention also claims for GITR-B
CC   (AAW49017) and GITR-C (AAW49018) which are splicing variants of GITR. The
CC   GITRs are claimed to be useful for stimulating lymphocyte activity and
CC   cell death rescue. GITR antagonists are claimed to be useful for
CC   suppressing the lymphocyte activity and for inducing apoptotic deletion.
CC   GITR cDNAs and the proteins they encode are also claimed to be useful for
CC   suppressing growth of tumour cells over-expressing GITR or for the
CC   treatment of refractory hodgkin's disease
XX
SQ   Sequence 228 AA;

  Query Match             100.0%;  Score 1301;  DB 2;  Length 228;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-112;
  Matches  228;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60

Qy         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120

Qy        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180

Qy        181 RRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP 228
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP 228


RESULT 3
ADA09440
ID   ADA09440 standard; protein; 228 AA.
XX
AC   ADA09440;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Murine GITR protein.
XX
KW   Tumour necrosis factor receptor-like protein; TNF receptor-like protein;
KW   TR11; TR11SV1; TR11SV2; cell proliferation; cell differentiation;
KW   cell mobilisation; immune cell; immune system disorder;
KW   haematopoietic cell disorder; pluripotent stem cell;
KW   blood protein disorder; HIV-infection; anaemia; thrombocytopaenia;
KW   thrombolytic activity; blood coagulation disorder;
KW   blood platelet disorder; wound; stoke; myocardial infarction; scarring;
KW   autoimmune disorder; allergic reaction; asthma; organ rejection;
KW   graft versus host disease; GVHD; hyperproliferative disorder; neoplasm;
KW   cancer; inflammatory condition; infectious disease;
KW   peripheral nervous system disease; spinal cord disorder;
KW   cerebrovascular disease; anti-HIV; antianaemic; haemostatic; vulnerary;
KW   cerebroprotective; cardiant; antirheumatic; antiarthritic; antiallergic;
KW   nephrotropic; antidiabetic; immunosuppressive; antiinflammatory;
KW   antithyroid; antiasthmatic; vasotropic; antibacterial; virucide;
KW   fungicide; antiparasitic; neuroprotective; nootropic; antiparkinsonian;
KW   anticonvulsant; murine;
KW   glucocorticoid-induced tumour necrosis factor receptor; GITR.
```

XX
OS Mus musculus.
XX
PN US6509173-B1.
XX
PD 21-JAN-2003.
XX
PF 21-OCT-1998; 98US-00176200.
XX
PR 21-OCT-1997; 97US-0063212P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ni J, Ruben SM;
XX
DR WPI; 2003-352290/33.
XX
PT Novel nucleic acids encoding human tumor necrosis factor receptor-like
PT proteins TR11, TR11SV1 and TR11SV2, useful for treating blood coagulation
PT disorders, blood platelet disorders, stroke and myocardial infarction.
XX
PS Disclosure; Fig 4; 70pp; English.
XX
CC The present invention relates to the isolation of novel human tumour
CC necrosis factor (TNF) receptor-like proteins, designated TR11, TR11SV1
CC and TR11SV2 receptors, and the polynucleotide sequences encoding them.
CC the polypeptide and polynucleotide sequences for TR11, TR11SV1,and
CC TR11SV2 are useful in assays to test one or more biological activities of
CC TR11, TR11SV1 and TR11SV2 polypeptides, for proliferation,
CC differentiation and mobilisation of immune cells, and as markers or
CC detectors of a particular immune system disease or disorder. They are
CC also useful in treating or detecting deficiencies or disorders of
CC haematopoietic cells, to increase differentiation and proliferation of
CC haematopoietic cells, including pluripotent stem cells in an effort to
CC treat disorders associated with a decrease in haematopoietic cells e.g.
CC blood protein disorders, HIV-infection, anaemia and thrombocytopaenia.
CC The sequences are also useful for modulating haemostatic or thrombolytic
CC activity, for treating blood coagulation disorders, blood platelet
CC disorders or wounds resulting from trauma, as well as for treating
CC stroke, myocardial infarction and scarring. They may be used for
CC detecting or treating autoimmune disorders (e.g. Addison's disease,
CC rheumatoid arthritis, dermatitis, allergic encephalomyelitis,
CC glomerulonephritis, Grave's disease, diabetes mellitus, multiple
CC sclerosis and autoimmune thyroiditis), for treating allergic reactions
CC such as asthma, for treating and/or preventing organ rejection or graft
CC versus host disease (GVHD), for treating hyperproliferative disorders
CC including neoplasms and cancers, for treating or modulating inflammation
CC or inflammatory conditions such as inflammation associated with infection
CC (e.g. septic shock and sepsis, ischaemia-reperfusion injury, endotoxin
CC lethality, induced lung injury and Crohn's disease), for treating or
CC detecting infectious agents such as viruses, bacteria, parasites and
CC fungi, for differentiating, proliferating and attracting cells for tissue
CC regeneration, and as vaccines to raise immune response against infectious
CC diseases. The polynucleotide sequences are also useful in ex vivo gene
CC therapy, and for proliferating and differentiating peripheral nervous
CC system diseases such as spinal cord disorders, cerebrovascular diseases,
CC Alzheimer's disease, Parkinson's disease, Huntington's disease,
CC amyotrophic lateral sclerosis and Shy-Drager syndrome. The present
CC sequence represents murine glucocorticoid-induced tumour necrosis factor
CC receptor family related protein (GITR).
XX
SQ Sequence 228 AA;

Query Match 100.0%; Score 1301; DB 6; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.6e-112;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60

Qy         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120

Qy        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180

Qy        181 RRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP 228
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP 228
```

RESULT 4
ADH43110
ID ADH43110 standard; protein; 228 AA.
XX
AC ADH43110;
XX
DT 25-MAR-2004 (first entry)
XX
DE Mouse glucocorticoid-induced tumour necrosis factor receptor (GITR).
XX
KW antiinflammatory; osteopathic; immunosuppressive; neuroprotective;
KW immunostimulant; antirheumatic; dermatological; antithyroid; haemostatic;
KW antiasthmatic; antiarthritic; cytostatic; proliferation inhibitor;
KW differentiation inhibitor; T-cell chemotaxis inhibitor;
KW B-cell chemotaxis inhibitor; haemostatsis; thrombolytic activity;
KW TR11SV1; TR11SV2; tumour necrosis factor receptor-like protein;
KW TNF receptor-like protein; inflammation; bone disease; Paget's disease;
KW osteopetrosis; craniometaphyseal dysplasia;
KW fibrodysplasia ossificans progressiva; gigantism; osteoclastoma;
KW autoimmune disorder; autoimmune haemolytic anaemia; autoimmunocytopenia;
KW multiple sclerosis; autoimmune thyroiditis; immunodeficiency disorder;
KW severe combined immunodeficiency; Wiskott-Aldrich syndrome;
KW rheumatoid arthritis; systemic lupus erythematosus;
KW graft-versus-host disease; asthma; cancer; Grave's disease;
KW blood coagulation disorder; platelet disorder; thrombocytopenia; TR11;
KW tumour necrosis factor receptor family; mouse;
KW glucocorticoid-induced tumour necrosis factor receptor; GITR.
XX
OS Mus musculus.
XX
PN US2003138426-A1.
XX
PD 24-JUL-2003.
XX
PF 30-OCT-2002; 2002US-00283105.
XX
PR 21-OCT-1997; 97US-0063212P.
PR 21-OCT-1998; 98US-00176200.
PR 24-FEB-1999; 99US-0121648P.
PR 13-MAY-1999; 99US-0134172P.
PR 16-JUL-1999; 99US-0144076P.
PR 23-FEB-2000; 2000US-00512363.
PR 28-JUL-2000; 2000US-0221577P.
PR 27-JUL-2001; 2001US-00915593.
PR 30-OCT-2001; 2001US-0330757P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ni J, Ruben SM;
XX
DR WPI; 2004-068938/07.
XX
PT Novel isolated antibody binding to TR11SV1/TR11SV2 receptor, useful for
PT treating inflammation, Paget's disease, thyroiditis.
XX
PS Disclosure; SEQ ID NO 7; 135pp; English.
XX
CC The invention describes an isolated antibody (I) or its portion
CC specifically binding to a protein chosen from a protein with amino acid
CC residues 1-62 or 51-62 of a fully defined TR11SV1 receptor sequence of
CC 241 amino acids (S1) as given in specification, and a protein with amino
CC acid residues 38-49 of a fully defined TR11SV2 receptor sequence of 240

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CC   amino acids as given in specification. (I) is useful for detecting tumour
CC   necrosis factor (TNF) receptor-like proteins TR11SV1 or TR11SV2 protein
CC   in a biological sample, which involves contacting the biological sample
CC   with (I), and detecting the TR11SV1 or TR11SV2 protein in the biological
CC   sample. (I) is a labeled antibody, the label is chosen from an enzyme
CC   label, a radioisotope, a fluorescent label, and biotin. The method
CC   described is useful for treating inflammation. Also described is a method
CC   useful for treating bone disease or a disorder such as Paget's disease,
CC   Osteopetrosis, craniometaphyseal dysplasia, fibrodysplasia ossificans
CC   progressiva, gigantism, or osteoclastoma. (I) is useful for treating
CC   autoimmune disorders e.g. autoimmune haemolytic anaemia,
CC   autoimmunocytopenia, multiple sclerosis, autoimmune thyroiditis, etc.,
CC   immunodeficiency disorders e.g. severe combined immunodeficiency and
CC   Wiskott-Aldrich syndrome. (I) is also useful for treating rheumatoid
CC   arthritis, systemic lupus erythematosus, graft-versus-host disease,
CC   asthma, cancer, Grave's disease, blood coagulation disorders and platelet
CC   disorders (thrombocytopenia). This is the amino acid sequence of mouse
CC   glucocorticoid-induced tumour necrosis factor receptor (GITR) used in a
CC   comparison with the novel tumour necrosis factor receptor family members
CC   TR11, TR11SV1 and TR11SV2.
XX
SQ   Sequence 228 AA;

  Query Match             100.0%;  Score 1301;  DB 8;  Length 228;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-112;
  Matches  228;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60

Qy         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120

Qy        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180

Qy        181 RRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP 228
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP 228


RESULT 5
AAW49018
ID   AAW49018 standard; protein; 222 AA.
XX
AC   AAW49018;
XX
DT   29-SEP-1998  (first entry)
XX
DE   Mouse glucocorticoid induced TNFR-family related protein variant C.
XX
KW   Mouse glucocorticoid induced TNFR-family related protein; lymphocyte;
KW   GITR; tumour necrosis factor; apoptosis; hodgkin's disease; GITR-B;
KW   GITR-C.
XX
OS   Mus sp.
XX
PN   WO9824895-A1.
XX
PD   11-JUN-1998.
XX
PF   08-NOV-1997;   97WO-EP006252.
XX
PR   02-DEC-1996;   96GB-00025074.
XX
PA   (PHAA ) PHARMACIA & UPJOHN SPA.
XX
PI   Riccardi C;
XX
DR   WPI; 1998-333315/29.
DR   N-PSDB; AAV32775.
XX
PT   New isolated glucocorticoid induced TNFR related polypeptide - used to
PT   stimulate lymphocyte activity and cell death rescue, useful to, e.g.
PT   develop products to suppress lymphocyte activity and induce apoptosis.
XX
PS   Claim 15; Page 43-44; 53pp; English.
XX
CC   The present claimed sequence represents a mouse glucocorticoid induced
CC   TNFR-family related protein variant C (GITR-C). The invention also claims
CC   for GITR (AAW49016) and GITR-B (AAW49017). The GITRs are claimed to be
CC   useful for stimulating lymphocyte activity and cell death rescue. GITR
CC   antagonists are claimed to be useful for suppressing the lymphocyte
CC   activity and for inducing apoptotic deletion. GITR cDNAs and the proteins
CC   they encode are also claimed to be useful for suppressing growth of
CC   tumour cells over-expressing GITR or for the treatment of refractory
CC   hodgkin's disease
XX
SQ   Sequence 222 AA;

  Query Match             82.9%;  Score 1079;  DB 2;  Length 222;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-92;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60

Qy         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120

Qy        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180

Qy        181 RRQHMCPR 188
              ||||||||
Db        181 RRQHMCPR 188


RESULT 6
AAW49017
ID   AAW49017 standard; protein; 294 AA.
XX
AC   AAW49017;
XX
DT   29-SEP-1998  (first entry)
XX
DE   Mouse glucocorticoid induced TNFR-family related protein variant B.
XX
KW   Mouse glucocorticoid induced TNFR-family related protein; lymphocyte;
KW   GITR; tumour necrosis factor; apoptosis; hodgkin's disease; GITR-B;
KW   GITR-C.
XX
OS   Mus sp.
XX
PN   WO9824895-A1.
XX
PD   11-JUN-1998.
XX
PF   08-NOV-1997;   97WO-EP006252.
XX
PR   02-DEC-1996;   96GB-00025074.
XX
PA   (PHAA ) PHARMACIA & UPJOHN SPA.
XX
PI   Riccardi C;
XX
DR   WPI; 1998-333315/29.
DR   N-PSDB; AAV32774.
XX
PT   New isolated glucocorticoid induced TNFR related polypeptide - used to
```

```
PT   stimulate lymphocyte activity and cell death rescue, useful to, e.g.
PT   develop products to suppress lymphocyte activity and induce apoptosis.
XX
PS   Claim 14; Page 40-41; 53pp; English.
XX
CC   The present claimed sequence represents a mouse glucocorticoid induced
CC   TNFR-family related protein variant B (GITR-B). The invention also claims
CC   for GITR (AAW49016) and GITR-C (AAW49018). The GITRs are claimed to be
CC   useful for stimulating lymphocyte activity and cell death rescue. GITR
CC   antagonists are claimed to be useful for suppressing the lymphocyte
CC   activity and for inducing apoptotic deletion. GITR cDNAs and the proteins
CC   they encode are also claimed to be useful for suppressing growth of
CC   tumour cells over-expressing GITR or for the treatment of refractory
CC   hodgkin's disease
XX
SQ   Sequence 294 AA;

  Query Match             82.9%;  Score 1079;  DB 2;  Length 294;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-92;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60

Qy         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120

Qy        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180

Qy        181 RRQHMCPR 188
              ||||||||
Db        181 RRQHMCPR 188


RESULT 7
ADR46662
ID   ADR46662 standard; protein; 240 AA.
XX
AC   ADR46662;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Cancer-associated protein, SEQ ID 75.
XX
KW   Cytostatic; Gene Therapy; cancer; human.
XX
OS   Homo sapiens.
XX
PN   WO2004073657-A2.
XX
PD   02-SEP-2004.
XX
PF   19-FEB-2004; 2004WO-US005455.
XX
PR   19-FEB-2003; 2003US-0448784P.
XX
PA   (PROT-) PROTEIN DESIGN LABS INC.
XX
PI   Aziz N,  Gish KC,  Wilson KE,  Zlotnik A;
XX
DR   WPI; 2004-652787/63.
DR   N-PSDB; ADR46604.
XX
PT   Detecting a pathological cell in a patient for diagnosing or treating
PT   cancer by detecting in a biological sample from the patient genes whose
PT   expression are up-regulated or down-regulated in specific cancers.
XX
PS   Claim 1; SEQ ID NO 75; 375pp; English.
XX
CC   The present invention relates to a method for detecting cancer in a
CC   patient. The method comprises detecting in a biological sample from the
CC   patient a nucleotide or protein sequence comprising a sequence that is at
CC   least 80% identical to a nucleotide sequence (ADR46588-ADR46645) or
CC   protein sequence (ADR46646-ADR46703). The method is useful for detecting
CC   cancer for preparing a composition for diagnosing or treating cancer.
XX
SQ   Sequence 240 AA;

  Query Match             56.5%;  Score 735.5;  DB 8;  Length 240;
  Best Local Similarity   57.0%;  Pred. No. 5.7e-60;
  Matches  134;  Conservative   31;  Mismatches   61;  Indels    9;  Gaps    3;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-------PGKE 53
              |||:  | |:::|| | |||       ||||||::  |:| : ||| ::        ||:|
Db          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65

Qy         54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
               | :  |:|| ||:|||||  |  |:|:|| ||| |:|||   |||:|: || |||| | :
Db         66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125

Qy        114 GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
              |||: ||:|:||||||:|||||||||||:|   | |  | |||: | :|||:  ||: ||
Db        126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQL 185

Qy        174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEKCHLGGRW 227
              |||||||| | | |||||   ||  | ||| | |||||||||:: |||  ||  |
Db        186 GLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240


RESULT 8
AAW37839
ID   AAW37839 standard; protein; 241 AA.
XX
AC   AAW37839;
XX
DT   28-JUL-1998  (first entry)
XX
DE   Amino acid sequence of the human 312C2 T cell protein.
XX
KW   Human 312C2 T cell protein; thymus cell; spleen cell; T cell;
KW   antigen-specific T cell proliferation; cytokine production by T-cell;
KW   apoptosis; cancer; haematopoietic cells; lymphoid cell;
KW   autoimmune disorders.
XX
OS   Homo sapiens.
XX
PN   WO9806842-A1.
XX
PD   19-FEB-1998.
XX
PF   14-AUG-1997;   97WO-US013931.
XX
PR   16-AUG-1996;   96US-00689943.
PR   07-OCT-1996;   96US-0027901P.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Gorman DM,  Randall TD,  Zlotnik A;
XX
DR   WPI; 1998-159534/14.
DR   N-PSDB; AAV19153.
XX
PT   Isolated 312C2 T cell gene - used to develop products for treating, e.g.
PT   cancers, auto-immune disorders, transplantation rejection and other T
PT   cell disorders.
XX
PS   Claim 2; Page 59-60; 71pp; English.
XX
CC   This is the amino acid sequence encoding the human 312C2 T cell protein.
CC   The 312C2 proteins are expressed in thymus cells and are induced on T
CC   cells and spleen cells following activation. Engagement of 312C2
CC   stimulates proliferation of T cell clones, antigen-specific proliferation
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CC   and cytokine production by T-cells, and potentiates T cell expansion or
CC   apoptosis. The products can be used in the treatment of conditions
CC   associated with abnormal physiology or development, including abnormal
CC   proliferation, e.g. cancerous conditions or degenerative conditions. They
CC   can be used in the regulation or development of haematopoietic cells,
CC   e.g. lymphoid cells which affect immunological responses, e.g. autoimmune
CC   disorders
XX
SQ   Sequence 241 AA;

  Query Match             56.5%;  Score 735.5;  DB 2;  Length 241;
  Best Local Similarity   57.0%;  Pred. No. 5.8e-60;
  Matches  134;  Conservative   31;  Mismatches   61;  Indels    9;  Gaps    3;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-------PGKE 53
              |||:  | |:::|| | |||      ||||||::  |:| : ||| ::        ||:|
Db          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65

Qy         54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
               | :  |:|| ||:||||| |  |:|:|| ||| |:|||   |||:|: || |||| | :
Db         66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125

Qy        114 GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
              |||: ||:|:|||||:||||||||||:|   | |  | |||: | :|||:  ||: ||
Db        126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQL 185

Qy        174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEKCHLGGRW 227
              |||||||| | | |||||   ||  | ||| | |||||||||:: |||  ||  |
Db        186 GLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240


RESULT 9
AAY06605
ID   AAY06605 standard; protein; 241 AA.
XX
AC   AAY06605;
XX
DT   26-OCT-1999  (first entry)
XX
DE   Human TNF receptor homologue PRO364.
XX
KW   PRO364; tumour necrosis factor receptor; human; apoptosis; inflammation;
KW   antiinflammatory; NF-KB activation; autoimmune disease; therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .25
FT                   /note= "signal peptide"
FT   Protein         26. .241
FT                   /note= "mature protein"
FT   Modified-site   146
FT                   /note= "N-glycosylated"
FT   Domain          162. .180
FT                   /note= "transmembrane domain"
XX
PN   WO9940196-A1.
XX
PD   12-AUG-1999.
XX
PF   09-FEB-1999;   99WO-US002642.
XX
PR   09-FEB-1998;   98US-0074087P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Gurney AL,  Marsters SA,  Pitti RM,  Wood WI;
PI   Goddard A;
XX
DR   WPI; 1999-494296/41.
DR   N-PSDB; AAX87670.
XX
PT   Tumor necrosis factor receptor homologue - useful for, e.g. modulating
PT   apoptosis and NF-KB activation and proinflammatory or autoimmune
PT   responses.
XX
PS   Claim 17; Fig 2A; 104pp; English.
XX
CC   The present sequence represents human PRO364, a novel member of the
CC   tumour necrosis factor receptor family. The sequence was deduced from a
CC   bone marrow cDNA clone (see AAX87670). Methods for the recombinant
CC   production of PRO364 polypeptides, e.g. in CHO, Escherichia coli or yeast
CC   host cells, are provided. Claimed polypeptides comprise amino acids 1-
CC   241, 1-X, 26-241 (i.e. the mature protein) and 26-X of the present
CC   sequence, where X is any one of amino acid respdies 157-167 of PRO364.
CC   PRO364 polypeptides are useful for modulating apoptosis, NF-KB activation
CC   and proinflammatory or autoimmune responses in mammalian cells (claimed).
CC   Chimeric molecules comprising a PRO364 polypeptide fused to a
CC   heterologous sequence such as epitope tag or immunoglobulin Fc region are
CC   also claimed. PRO364 can be used in assays to identify other proteins or
CC   molecules involved in binding interactions. This is useful for
CC   identifying inhibitors or agonists of receptor/ligand binding. The PRO364
CC   polypeptides may also be combined with an agent that is cytotoxic,
CC   chemotherapeutic or a growth inhibitor. PRO364 antibodies are useful in
CC   diagnostic methods, purification methods and also in therapy, e.g. as
CC   inhibitors
XX
SQ   Sequence 241 AA;

  Query Match             56.5%;  Score 735.5;  DB 2;  Length 241;
  Best Local Similarity   57.0%;  Pred. No. 5.8e-60;
  Matches  134;  Conservative   31;  Mismatches   61;  Indels    9;  Gaps    3;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-------PGKE 53
              |||:  | |:::|| | |||      ||||||::  |:| : ||| ::        ||:|
Db          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65

Qy         54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
               | :  |:|| ||:||||| |  |:|:|| ||| |:|||   |||:|: || |||| | :
Db         66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125

Qy        114 GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
              |||: ||:|:|||||:||||||||||:|   | |  | |||: | :|||:  ||: ||
Db        126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQL 185

Qy        174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEKCHLGGRW 227
              |||||||| | | |||||   ||  | ||| | |||||||||:: |||  ||  |
Db        186 GLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240


RESULT 10
AAB33431
ID   AAB33431 standard; protein; 241 AA.
XX
AC   AAB33431;
XX
DT   29-JAN-2001  (first entry)
XX
DE   Human PRO364 protein UNQ319 SEQ ID NO:92.
XX
KW   Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW   dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW   haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW   antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW   antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW   osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW   idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW   systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW   autoimmune thrombocytopaenia; immune-mediated renal disease;
KW   demyelinating disease; hepatobiliary disease; Whipple's disease;
KW   inflammatory bowel disease; gluten-sensitive enteropathy;
KW   autoimmune disease; immune-mediated skin disease; allergic disease;
KW   immunological disease; transplantation associated disease;
KW   graft rejection; graft-versus-host-disease.
XX
OS   Homo sapiens.
```

```
XX
PN   WO200053758-A2.
XX
PD   14-SEP-2000.
XX
PF   02-MAR-2000; 2000WO-US005841.
XX
PR   08-MAR-1999;   99WO-US005028.
PR   10-MAR-1999;   99US-0123618P.
PR   12-MAR-1999;   99US-0123957P.
PR   23-MAR-1999;   99US-0125775P.
PR   12-APR-1999;   99US-0128849P.
PR   20-APR-1999;   99WO-US008615.
PR   28-APR-1999;   99US-0131445P.
PR   04-MAY-1999;   99US-0132371P.
PR   14-MAY-1999;   99US-0134287P.
PR   02-JUN-1999;   99WO-US012252.
PR   23-JUN-1999;   99US-0141037P.
PR   20-JUL-1999;   99US-0144758P.
PR   26-JUL-1999;   99US-0145698P.
PR   28-JUL-1999;   99US-0146222P.
PR   01-SEP-1999;   99WO-US020111.
PR   08-SEP-1999;   99WO-US020594.
PR   13-SEP-1999;   99WO-US020944.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   05-OCT-1999;   99WO-US023089.
PR   29-OCT-1999;   99US-0162506P.
PR   29-NOV-1999;   99WO-US028214.
PR   30-NOV-1999;   99WO-US028313.
PR   30-NOV-1999;   99WO-US028409.
PR   01-DEC-1999;   99WO-US028301.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028564.
PR   02-DEC-1999;   99WO-US028565.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030999.
PR   30-DEC-1999;   99WO-US031274.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000277.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Goddard A,  Gurney AL,  Hebert C,  Henzel W;
PI   Kabakoff RC,  Lu Y,  Pan J,  Pennica D,  Shelton DL,  Smith V;
PI   Stewart TA,  Tumas D,  Watanabe CK,  Wood WI,  Yan M;
XX
DR   WPI; 2000-572271/53.
DR   N-PSDB; AAC58596.
XX
PT   Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT   immune related disorders, e.g. systemic lupus erythematosis, rheumatoid
PT   arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
XX
PS   Claim 33; Fig 36; 309pp; English.
XX
CC   The present invention describes sixty four human PRO proteins which can
CC   be used in the treatment of immune related diseases. The human PRO
CC   proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC   treating and diagnosing immune related disorders. The disorders are
CC   selected from systemic lupus erythematosus, rheumatoid arthritis,
CC   osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC   systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC   syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC   anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC   immune-mediated renal disease, demyelinating diseases of the central and
CC   peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
CC   disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
CC   or immune-mediated skin diseases, allergic diseases, immunological
CC   diseases of the lung, and transplantation associated diseases including
CC   graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
CC   represent PCR primers and hybridisation probes used in the isolation of
CC   human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
CC   represent human PRO polynucleotide and protein sequences given in the
CC   exemplification of the present invention
XX
SQ   Sequence 241 AA;

  Query Match             56.5%;  Score 735.5;  DB 3;  Length 241;
  Best Local Similarity   57.0%;  Pred. No. 5.8e-60;
  Matches  134;  Conservative   31;  Mismatches   61;  Indels    9;  Gaps    3;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-------PGKE 53
              |||:  | |:::|| | |||      ||||||::  |:| : ||| ::         ||:|
Db          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65

Qy         54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
               | :  |:|| ||:|||| |  |:|:|| ||| |:|||   |||:|: || |||| | :
Db         66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125

Qy        114 GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
              |||: ||:|:||||||:||||||||||:|    | |  | |||: | :|||:  ||: ||
Db        126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQL 185

Qy        174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEKCHLGGRW 227
              |||||||| | | |||||   ||  | ||| | |||||||||:: |||  ||  |
Db        186 GLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240


RESULT 11
AAY71467
ID   AAY71467 standard; protein; 241 AA.
XX
AC   AAY71467;
XX
DT   08-NOV-2000  (first entry)
XX
DE   Human PRO364 protein.
XX
KW   PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative;
KW   neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour;
KW   breast; prostate; colon; lung; renal; ovarian; central nervous system;
KW   CNS; leukemia; melanoma; Expressed Sequence Tag; EST; TNFR homologue;
KW   tumour necrosis factor receptor; GITR protein homologue.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .25
FT                   /label= Signal_peptide
FT   Modified-site   5. .11
FT                   /note= "N-myristoylation site"
FT   Modified-site   8. .14
FT                   /note= "N-myristoylation site"
FT   Modified-site   25. .31
FT                   /note= "N-myristoylation site"
FT   Protein         26. .241
FT                   /label= Mature_PRO364_protein
FT   Modified-site   30. .36
FT                   /note= "N-myristoylation site"
FT   Modified-site   33. .39
FT                   /note= "N-myristoylation site"
FT   Modified-site   118. .124
FT                   /note= "N-myristoylation site"
FT   Modified-site   122. .128
FT                   /note= "N-myristoylation site"
FT   Modified-site   146. .150
FT                   /note= "Asn is N-glycosylated"
FT   Modified-site   156. .162
FT                   /note= "N-myristoylation site"
```

```
FT   Domain          163. .183
FT                   /label= Transmembrane_domain
FT   Binding-site    166. .177
FT                   /note= "Prokaryotic membrane lipoprotein lipid attachment
FT                   site"
FT   Region          171. .193
FT                   /note= "Leucine zipper pattern"
XX
PN   WO200032778-A2.
XX
PD   08-JUN-2000.
XX
PF   30-NOV-1999;   99WO-US028409.
XX
PR   01-DEC-1998;   98WO-US025108.
PR   16-DEC-1998;   98US-0112850P.
PR   22-DEC-1998;   98US-0113296P.
PR   20-JUL-1999;   99US-0144758P.
PR   26-JUL-1999;   99US-0145698P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Chen J,  Goddard A,  Gurney AL,  Hillan K,  Napier M,  Wood WI;
XX
DR   WPI; 2000-412325/35.
DR   N-PSDB; AAD01240.
XX
PT   New composition useful for inhibiting neoplastic cell growth and for
PT   treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or their
PT   antagonists.
XX
PS   Claim 31; Fig 4; 108pp; English.
XX
CC   The present sequence is the human PRO364 protein, encoded by the cDNA
CC   clone, designated as DNA47365-1206. It is isolated from human small
CC   intestine tissue cDNA library, identified using probes based on the
CC   consensus sequence DNA44825, relative to the Incyte expressed sequence
CC   tag (EST) 3003460. This EST has homology to tumour necrosis factor
CC   receptor (TNFR) family of polypeptides. PRO364 sequence also shows
CC   homology to members of the TNFR family and mouse GITR protein. This clone
CC   is assigned the ATCC deposit No: 209436. PRO364 functions as a neoplastic
CC   cell growth inhibitor and is used for treating tumours, using an
CC   effective amount of PRO655, PRO364 and PRO344. This composition is
CC   especially useful for treatment of human cancers such as breast,
CC   prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma
XX
SQ   Sequence 241 AA;

  Query Match             56.5%;  Score 735.5;  DB 3;  Length 241;
  Best Local Similarity   57.0%;  Pred. No. 5.8e-60;
  Matches  134;  Conservative   31;  Mismatches   61;  Indels    9;  Gaps    3;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-------PGKE 53
              |||:  | |:::|| | |||      ||||||::  |:| : ||| ::        ||:|
Db          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65

Qy         54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
                | :  |:|| ||:||||| |  |:|:|| ||| |:|||   |||:|: || |||| | :
Db         66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125

Qy        114 GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
              |||: ||:|:||||||:|||||||||||:|   | |  | |||: | :|||:  ||: ||
Db        126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQL 185

Qy        174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEKCHLGGRW 227
              |||||||| | | |||||    ||  | ||| | |||||||||:: |||  ||  |
Db        186 GLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240


RESULT 12
AAB27651
ID   AAB27651 standard; protein; 241 AA.
XX
AC   AAB27651;
XX
DT   26-JAN-2001  (first entry)
XX
DE   Human protein PRO364.
XX
KW   Cardiovascular; endothelial; angiogenic disorder; PRO179; PRO238; PRO364;
KW   PRO844; PRO846; PRO1760; PRO205; PRO321; PRO333; PRO840; PRO877; PRO878;
KW   PRO879; PRO882; PRO885; PRO887; gene therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .25
FT                   /label= Signal peptide
XX
PN   WO200053757-A2.
XX
PD   14-SEP-2000.
XX
PF   24-FEB-2000; 2000WO-US005004.
XX
PR   08-MAR-1999;   99WO-US005028.
PR   12-MAR-1999;   99US-0123957P.
PR   02-JUN-1999;   99WO-US012252.
PR   20-JUL-1999;   99US-0144758P.
PR   26-JUL-1999;   99US-0145698P.
PR   01-SEP-1999;   99WO-US020111.
PR   15-SEP-1999;   99WO-US021090.
PR   30-NOV-1999;   99WO-US028313.
PR   30-NOV-1999;   99WO-US028409.
PR   02-DEC-1999;   99WO-US028565.
PR   05-JAN-2000; 2000WO-US000219.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Ferrara N,  Gerber H,  Gerritsen ME;
PI   Goddard A,  Gurney AL,  Hillan KJ,  Marsters SA,  Paoni NF,  Pitti RM;
PI   Watanabe CK,  Williams PM,  Wood WI;
XX
DR   WPI; 2000-611444/58.
DR   N-PSDB; AAA99903.
XX
PT   Novel PRO polypeptides and agonists and antagonists of them, used to
PT   diagnose and treat cardiovascular, endothelial and angiogenic disorders.
XX
PS   Claim 71; Fig 6; 181pp; English.
XX
CC   The present invention relates to methods for stimulating or inhibiting
CC   angiogenesis and cardiovascularization. The methods involve the use of
CC   pharmaceutical compositions based on the following proteins, PRO179,
CC   PRO238, PRO364, PRO844, PRO846, PRO1760, PRO205, PRO321, PRO333, PRO840,
CC   PRO877, PRO878, PRO879, PRO882, PRO885 or PRO887. These proteins were
CC   identified by isolating cDNA clones encoding secreted proteins. The
CC   proteins of the invention may be used to diagnose and treat
CC   cardiovascular, endothelial or angiogenic disorders. The present sequence
CC   is one of the proteins of the invention
XX
SQ   Sequence 241 AA;

  Query Match             56.5%;  Score 735.5;  DB 3;  Length 241;
  Best Local Similarity   57.0%;  Pred. No. 5.8e-60;
  Matches  134;  Conservative   31;  Mismatches   61;  Indels    9;  Gaps    3;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-------PGKE 53
              |||:  | |:::|| | |||      ||||||::  |:| : ||| ::        ||:|
Db          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65

Qy         54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
                | :  |:|| ||:||||| |  |:|:|| ||| |:|||   |||:|: || |||| | :
```

```
Db         66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125

Qy        114 GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
              |||: ||:|:|||||||:|||||||||||:|   | |  | |||: | :|||:  ||: ||
Db        126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQL 185

Qy        174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEKCHLGGRW 227
              |||||||| | | |||||    ||   | ||| | |||||||||:: |||  ||  |
Db        186 GLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
```

RESULT 13
AAY95895
ID AAY95895 standard; protein; 241 AA.
XX
AC AAY95895;
XX
DT 20-NOV-2000 (first entry)
XX
DE Human tumour necrosis factor receptor-like protein TR11 mutein.
XX
KW TR11; human; tumour necrosis factor receptor-like protein;
KW immunodeficiency; autoimmune disease; rheumatoid arthritis;
KW immunosuppressive; antirheumatic; antiarthritic; haemostatic;
KW dermatological; antiinflammatory; therapy; diagnosis; mutein; mutant.
XX
OS Homo sapiens.
XX
PN WO200050459-A1.
XX
PD 31-AUG-2000.
XX
PF 23-FEB-2000; 2000WO-US004572.
XX
PR 24-FEB-1999; 99US-0121648P.
PR 13-MAY-1999; 99US-0134172P.
PR 16-JUL-1999; 99US-0144076P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Ni J;
XX
DR WPI; 2000-572072/53.
XX
PT Human tumor necrosis factor receptor-like proteins useful for diagnosis,
PT prevention and treatment of disease states associated with aberrant cell
PT survival such as autoimmune disease and rheumatoid arthritis.
XX
PS Disclosure; 294-295; 278pp; English.
XX
CC The present sequence is that of human tumour necrosis factor receptor-
CC like protein TR11 (see also AAY95879), a novel protein showing identity
CC to murine glucocorticoid induced tumour necrosis factor receptor family-
CC related gene. The invention provides highly conserved TR11, TR11SV1 and
CC TR11SV2 proteins (see AAY95879-81), as well as vectors, host cells and
CC recombinant methods for their production. TR11, TR11SV1 and/or TR11SV2
CC polypeptides are useful for treating, preventing, prognosis and/or
CC diagnosis of an immunodeficiency, especially common variable
CC immunodeficiency, X-linked agammaglobulinemia, severe combined
CC immunodeficiency (SCID), Wiskott-Aldrich syndrome or X-linked
CC immunoglobulin deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2
CC antagonists (e.g. antibodies) are used to treat, prevent, prognose and/or
CC diagnose an autoimmune disease, especially rheumatoid arthritis, systemic
CC lupus erythematosus, thrombocytopenia purpura or IgA nephropathy. The
CC polypeptides, polynucleotides and/or antibodies can be administered to
CC cells in vitro, ex vivo or in vivo or to a multicellular organism.
CC Soluble forms of the polypeptides may also be used. Methods for screening
CC for agonist/antagonist compounds are also provided
XX
SQ Sequence 241 AA;

Query Match 56.5%; Score 735.5; DB 3; Length 241;
Best Local Similarity 57.0%; Pred. No. 5.8e-60;
Matches 134; Conservative 31; Mismatches 61; Indels 9; Gaps 3;

```
Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-------PGKE 53
              |||:  | |:::|| | |||        ||||||::  |:| : ||| ::        ||:|
Db          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65

Qy         54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
               | :  |:|| ||:|||||  |  |:|:|| ||| |:|||   |||:|: || |||| | :
Db         66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125

Qy        114 GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
              |||: ||:|:|||||||:|||||||||||:|   | |  | |||: | :|||:  ||: ||
Db        126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQL 185

Qy        174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEKCHLGGRW 227
              |||||||| | | |||||    ||   | ||| | |||||||||:: |||  ||  |
Db        186 GLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
```

RESULT 14
AAB24409
ID AAB24409 standard; protein; 241 AA.
XX
AC AAB24409;
XX
DT 07-NOV-2000 (first entry)
XX
DE Human PRO364 protein sequence SEQ ID NO:117.
XX
KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;
KW cytostatic; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
PN WO200032221-A2.
XX
PD 08-JUN-2000.
XX
PF 30-NOV-1999; 99WO-US028313.
XX
PR 01-DEC-1998; 98WO-US025108.
PR 16-DEC-1998; 98US-0112850P.
PR 12-JAN-1999; 99US-0115554P.
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 28-APR-1999; 99US-0131445P.
PR 14-MAY-1999; 99US-0134287P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-OCT-1999; 99US-0162506P.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;
PI Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;
PI Smith V, Watanabe CK, Williams PM, Wood WI;
XX
DR WPI; 2000-412154/35.
DR N-PSDB; AAA77604.
XX
PT Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing
PT and treating diagnosing a cardiovascular, endothelial or angiogenic
PT disorders in mammals.

```
XX
PS   Claim 72; Fig 44; 315pp; English.
XX
CC   The present invention describes nucleic acids encoding PRO polypeptides
CC   useful for preventing, diagnosing and treating diagnosing a
CC   cardiovascular, endothelial or angiogenic disorder in mammals by
CC   modulating cell proliferation, angiogenesis and cardiovascularisation,
CC   and for identifying agonists and antagonists of these processes. The
CC   nucleic acids and the proteins they encode may be used in the prevention,
CC   treatment and diagnosis of diseases associated with inappropriate PRO
CC   expression such as cardiovascular, endothelial or angiogenic disorders in
CC   mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For
CC   example, the nucleic acids (NCs) and vectors containing them and the PRO
CC   polypeptide may be used to treat disorders associated with decreased PRO
CC   expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent
CC   nucleotide and protein sequences used in the exemplification of the
CC   present invention
XX
SQ   Sequence 241 AA;

  Query Match             56.5%;  Score 735.5;  DB 3;  Length 241;
  Best Local Similarity   57.0%;  Pred. No. 5.8e-60;
  Matches  134;  Conservative   31;  Mismatches   61;  Indels    9;  Gaps    3;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-------PGKE 53
              |||:  | |:::|| | |||      ||||||::  |:| : ||| ::        ||:|
Db          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65

Qy         54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
               | :  |:|| ||:|||| |  |:|:|| ||| |:|||   |||:|: || |||| | :
Db         66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125

Qy        114 GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
              |||: ||:|:|||||:|||||||||||:|   | |  | |||: | :|||:  ||: ||
Db        126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQL 185

Qy        174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEKCHLGGRW 227
              |||||||| | | |||||   ||  | ||| | |||||||||:: |||  ||  |
Db        186 GLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240


RESULT 15
AAB47054
ID   AAB47054 standard; protein; 241 AA.
XX
AC   AAB47054;
XX
DT   08-MAY-2001  (first entry)
XX
DE   Human PRO364.
XX
KW   PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor;
KW   hGITR; ligand; hGITRL; PRO175; tumour necrosis factor receptor; TNFR;
KW   human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy;
KW   myocardial infarction; PGF_2alpha; trauma; cancer; angiogenesis;
KW   age-related macular degeneration; antibody; periodontal disease;
KW   vascular-related drug targeting; atherosclerosis; hypertension;
KW   inflammatory vasculitides; Reynaud's disease; aneurysm;
KW   arterial restenosis; thrombophlebitis; tumor angiogenesis; lung; liver;
KW   fibrosis; neuropathy; rheumatoid arthritis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .26
FT                   /note= "Potential signal peptide"
FT   Modified-site   146
FT                   /note= "N-glycosylated"
FT   Domain          162. .180
FT                   /note= "Potential transmembrane domain"
XX
PN   WO200103720-A2.
XX
PD   18-JAN-2001.
XX
PF   11-JUL-2000; 2000WO-US018867.
XX
PR   12-JUL-1999;   99US-0143304P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Williams PM,  Gerritsen ME;
XX
DR   WPI; 2001-138257/14.
DR   N-PSDB; AAC85433.
XX
PT   Composition for diagnosing and treating cardiovascular, endothelial and
PT   angiogenic disorders, comprises a PRO364 or PRO175 polypeptide.
XX
PS   Claim 1; Fig 1; 76pp; English.
XX
CC   This sequence represents PRO364 polypeptide, which is a human gluco-
CC   corticoid-induced tumor necrosis factor receptor (hGITR). The
CC   corresponding ligand (hGITRL), PRO175, is given in AAB47056. PRO364 and
CC   PRO175 may be used in a mixture with a cardiovascular, endothelial,
CC   angiogenic or angiostatic agent for the treatment of a cardiovascular,
CC   endothelial, angiogenic or angiostatic disorder. The PRO364 cDNA sequence
CC   was isolated from an expressed sequence tag (EST) database as having
CC   homology to members of the tumour necrosis factor receptor (TNFR) family
CC   of polypeptides. The PRO175 cDNA sequence was isolated from a library of
CC   cDNA fragments derived from human umbilical vein endothelial cells
CC   (HUVEC). Administering an effective amount of PRO364 or PRO175 or their
CC   antagonists is useful for treating cardiac hypertrophy (which is
CC   initiated by myocardial infarction and characterized by the presence of
CC   an elevated level of PGF_2alpha), trauma, a cancer, or age-related
CC   macular degeneration in a human. Administering a therapeutically
CC   effective amount of an antibody that binds PRO364 or PRO175 is useful for
CC   inhibiting angiogenesis induced by PRO364 or PRO175 in a human suffering
CC   from a tumor or a retinal disorder. PRO364 or PRO175, or their
CC   antagonists, are useful for vascular-related drug targeting or as
CC   therapeutic targets for the treatment or prevention of atherosclerosis,
CC   hypertension, inflammatory vasculitides, Reynaud's disease, aneurysms,
CC   arterial restenosis, thrombophlebitis, tumor angiogenesis, gut protection
CC   or regeneration and treatment of lung or liver fibrosis, periodontal
CC   diseases, attraction of bone-forming cells, central and peripheral
CC   nervous system disease and neuropathies and rheumatoid arthritis
XX
SQ   Sequence 241 AA;

  Query Match             56.5%;  Score 735.5;  DB 4;  Length 241;
  Best Local Similarity   57.0%;  Pred. No. 5.8e-60;
  Matches  134;  Conservative   31;  Mismatches   61;  Indels    9;  Gaps    3;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-------PGKE 53
              |||:  | |:::|| | |||      ||||||::  |:| : ||| ::        ||:|
Db          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65

Qy         54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
               | :  |:|| ||:|||| |  |:|:|| ||| |:|||   |||:|: || |||| | :
Db         66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125

Qy        114 GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
              |||: ||:|:|||||:|||||||||||:|   | |  | |||: | :|||:  ||: ||
Db        126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQL 185

Qy        174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEKCHLGGRW 227
              |||||||| | | |||||   ||  | ||| | |||||||||:: |||  ||  |
Db        186 GLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240


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Job time : 140.689 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 26, 2005, 15:40:08 ; Search time 28.6823 Seconds
(without alignments)
593.397 Million cell updates/sec

Title: US-09-545-998B-2
Perfect score: 1301
Sequence: 1 MGAWAMLYGVSMLCVLDLGQ.....PEEERGEQTEEKCHLGGRWP 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1301	100.0	228	3	US-08-911-423-2	Sequence 2, Appli
2	1301	100.0	228	4	US-09-512-363-7	Sequence 7, Appli
3	1301	100.0	228	4	US-09-176-200-7	Sequence 7, Appli
4	1301	100.0	228	4	US-09-915-593-7	Sequence 7, Appli
5	735.5	56.5	241	3	US-08-911-423-4	Sequence 4, Appli
6	735.5	56.5	241	4	US-09-512-363-28	Sequence 28, Appl
7	735.5	56.5	241	4	US-09-915-593-28	Sequence 28, Appl
8	735.5	56.5	241	4	US-09-949-016-7232	Sequence 7232, Ap
9	703	54.0	228	3	US-08-911-423-6	Sequence 6, Appli
10	703	54.0	234	4	US-09-512-363-2	Sequence 2, Appli
11	703	54.0	234	4	US-09-176-200-2	Sequence 2, Appli
12	703	54.0	234	4	US-09-915-593-2	Sequence 2, Appli
13	697	53.6	240	4	US-09-512-363-6	Sequence 6, Appli
14	697	53.6	240	4	US-09-176-200-6	Sequence 6, Appli
15	697	53.6	240	4	US-09-915-593-6	Sequence 6, Appli
16	632.5	48.6	311	3	US-08-911-423-8	Sequence 8, Appli
17	630.5	48.5	241	4	US-09-512-363-4	Sequence 4, Appli
18	630.5	48.5	241	4	US-09-176-200-4	Sequence 4, Appli
19	630.5	48.5	241	4	US-09-915-593-4	Sequence 4, Appli
20	518	39.8	89	3	US-09-188-930-191	Sequence 191, App
21	518	39.8	89	4	US-09-312-283C-191	Sequence 191, App
22	287	22.1	232	3	US-08-911-423-7	Sequence 7, Appli
23	228.5	17.6	255	1	US-08-236-918A-8	Sequence 8, Appli
24	228.5	17.6	255	2	US-08-816-605-9	Sequence 9, Appli
25	228.5	17.6	255	3	US-09-006-353A-11	Sequence 11, Appl
26	228.5	17.6	255	3	US-09-007-097-2	Sequence 2, Appli
27	228.5	17.6	255	3	US-09-150-864A-8	Sequence 8, Appli
28	228.5	17.6	255	4	US-09-573-986-11	Sequence 11, Appl
29	228.5	17.6	255	4	US-09-578-764A-2	Sequence 2, Appli
30	228.5	17.6	255	4	US-09-623-545A-2	Sequence 2, Appli
31	228.5	17.6	255	5	PCT-US96-03965-8	Sequence 8, Appli
32	228.5	17.6	272	4	US-09-949-016-7520	Sequence 7520, Ap
33	222.5	17.1	219	2	US-08-816-605-2	Sequence 2, Appli
34	203.5	15.6	256	1	US-08-236-918A-6	Sequence 6, Appli
35	203.5	15.6	256	3	US-09-150-864A-6	Sequence 6, Appli
36	203.5	15.6	256	3	US-08-012-269A-2	Sequence 2, Appli
37	203.5	15.6	256	4	US-09-623-545A-3	Sequence 3, Appli
38	203.5	15.6	256	5	PCT-US96-03965-2	Sequence 2, Appli
39	162	12.5	191	3	US-08-974-022-52	Sequence 52, Appl
40	162	12.5	191	3	US-08-795-445A-52	Sequence 52, Appl
41	162	12.5	191	3	US-08-795-447A-52	Sequence 52, Appl
42	162	12.5	191	3	US-08-974-186-52	Sequence 52, Appl
43	162	12.5	191	3	US-08-795-446B-52	Sequence 52, Appl
44	162	12.5	191	3	US-08-706-945D-139	Sequence 139, App
45	162	12.5	191	4	US-08-577-788C-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1
US-08-911-423-2
; Sequence 2, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-911-423-2

Query Match 100.0%; Score 1301; DB 3; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.8e-121;

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  Matches  228;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60

Qy         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120
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Db         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120

Qy        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180

Qy        181 RRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP 228
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Db        181 RRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP 228


RESULT 2
US-09-512-363-7
; Sequence 7, Application US/09512363
; Patent No. 6503184
; GENERAL INFORMATION:
;  APPLICANT: Ni, Jian
;  APPLICANT: Ruben, Steven M.
;  TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
;  TITLE OF INVENTION: TR11, TR11SV1, and TR11SV2
;  FILE REFERENCE: PF396
;  CURRENT APPLICATION NUMBER: US/09/512,363
;  CURRENT FILING DATE: 2000-02-23
;  EARLIER APPLICATION NUMBER: 60/063,212
;  EARLIER FILING DATE: 1997-10-21
;  EARLIER APPLICATION NUMBER: 09/176,200
;  EARLIER FILING DATE: 1998-10-21
;  EARLIER APPLICATION NUMBER: 60/121,648
;  EARLIER FILING DATE: 1999-02-24
;  EARLIER APPLICATION NUMBER: 60/134,172
;  EARLIER FILING DATE: 1999-05-13
;  EARLIER APPLICATION NUMBER: 60/144,076
;  EARLIER FILING DATE: 1999-07-16
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 228
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-512-363-7

  Query Match           100.0%;  Score 1301;  DB 4;  Length 228;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-121;
  Matches  228;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60
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Db          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60

Qy         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120

Qy        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180

Qy        181 RRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP 228
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP 228


RESULT 3
US-09-176-200-7
; Sequence 7, Application US/09176200
; Patent No. 6509173
; GENERAL INFORMATION:
;  APPLICANT: Ni, Jian
;  APPLICANT: Ruben, Steven M.
;  TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
;  TITLE OF INVENTION: TR11, TR11SV1, and TR11SV2
;  FILE REFERENCE: PF396
;  CURRENT APPLICATION NUMBER: US/09/176,200
;  CURRENT FILING DATE: 1998-10-21
;  EARLIER APPLICATION NUMBER: 60/063,212
;  EARLIER FILING DATE: 1997-10-21
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 228
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-176-200-7

  Query Match           100.0%;  Score 1301;  DB 4;  Length 228;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-121;
  Matches  228;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60

Qy         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120

Qy        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180

Qy        181 RRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP 228
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP 228


RESULT 4
US-09-915-593-7
; Sequence 7, Application US/09915593
; Patent No. 6689607
; GENERAL INFORMATION:
;  APPLICANT: Ni, Jian
;  APPLICANT:  Ruben, Steven M.
;  TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
;  TITLE OF INVENTION:  TR11, TR11SV1, and TR11SV2
;  FILE REFERENCE: PF396P2
;  CURRENT APPLICATION NUMBER: US/09/915,593
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/221,577
;  PRIOR FILING DATE: 2000-07-28
;  PRIOR APPLICATION NUMBER: 09/512,363
;  PRIOR FILING DATE: 2000-02-23
;  PRIOR APPLICATION NUMBER: 60/144,076
;  PRIOR FILING DATE: 2000-07-16
;  PRIOR APPLICATION NUMBER: 60/134,172
;  PRIOR FILING DATE: 1999-05-13
;  PRIOR APPLICATION NUMBER: 60/121,648
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 09/176,200
;  PRIOR FILING DATE: 1998-10-21
;  PRIOR APPLICATION NUMBER: 60/063,212
;  PRIOR FILING DATE: 1997-10-21
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 228
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-915-593-7
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  Query Match           100.0%;  Score 1301;  DB 4;  Length 228;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-121;
  Matches  228;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60

Qy         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120

Qy        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180

Qy        181 RRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP 228
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP 228
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RESULT 5
US-08-911-423-4
; Sequence 4, Application US/08911423
; Patent No. 6111090
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Randall, Troy D.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,423
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/023,419
; FILING DATE: 16-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0612K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-911-423-4

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  Query Match           56.5%;  Score 735.5;  DB 3;  Length 241;
  Best Local Similarity  57.0%;  Pred. No. 3.1e-65;
  Matches  134;  Conservative   31;  Mismatches   61;  Indels    9;  Gaps    3;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-------PGKE 53
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Db          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65

Qy         54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
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Db         66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125

Qy        114 GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
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Db        126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQL 185

Qy        174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEKCHLGGRW 227
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Db        186 GLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
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RESULT 6
US-09-512-363-28
; Sequence 28, Application US/09512363
; Patent No. 6503184
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
; TITLE OF INVENTION: TR11, TR11SV1, and TR11SV2
; FILE REFERENCE: PF396
; CURRENT APPLICATION NUMBER: US/09/512,363
; CURRENT FILING DATE: 2000-02-23
; EARLIER APPLICATION NUMBER: 60/063,212
; EARLIER FILING DATE: 1997-10-21
; EARLIER APPLICATION NUMBER: 09/176,200
; EARLIER FILING DATE: 1998-10-21
; EARLIER APPLICATION NUMBER: 60/121,648
; EARLIER FILING DATE: 1999-02-24
; EARLIER APPLICATION NUMBER: 60/134,172
; EARLIER FILING DATE: 1999-05-13
; EARLIER APPLICATION NUMBER: 60/144,076
; EARLIER FILING DATE: 1999-07-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-512-363-28

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  Query Match           56.5%;  Score 735.5;  DB 4;  Length 241;
  Best Local Similarity  57.0%;  Pred. No. 3.1e-65;
  Matches  134;  Conservative   31;  Mismatches   61;  Indels    9;  Gaps    3;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-------PGKE 53
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Db          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65

Qy         54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
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Db         66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125

Qy        114 GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
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Db        126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQL 185

Qy        174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEKCHLGGRW 227
              |||||||| | | |||||   ||  | ||| | |||||||||:: |||  ||  |
Db        186 GLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
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RESULT 7
US-09-915-593-28
; Sequence 28, Application US/09915593
; Patent No. 6689607

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; GENERAL INFORMATION:
;  APPLICANT: Ni, Jian
;  APPLICANT:  Ruben, Steven M.
;  TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
;  TITLE OF INVENTION:  TR11, TR11SV1, and TR11SV2
;  FILE REFERENCE: PF396P2
;  CURRENT APPLICATION NUMBER: US/09/915,593
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/221,577
;  PRIOR FILING DATE: 2000-07-28
;  PRIOR APPLICATION NUMBER: 09/512,363
;  PRIOR FILING DATE: 2000-02-23
;  PRIOR APPLICATION NUMBER: 60/144,076
;  PRIOR FILING DATE: 2000-07-16
;  PRIOR APPLICATION NUMBER: 60/134,172
;  PRIOR FILING DATE: 1999-05-13
;  PRIOR APPLICATION NUMBER: 60/121,648
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 09/176,200
;  PRIOR FILING DATE: 1998-10-21
;  PRIOR APPLICATION NUMBER: 60/063,212
;  PRIOR FILING DATE: 1997-10-21
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
;   LENGTH: 241
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-915-593-28

  Query Match             56.5%;  Score 735.5;  DB 4;  Length 241;
  Best Local Similarity   57.0%;  Pred. No. 3.1e-65;
  Matches  134;  Conservative   31;  Mismatches   61;  Indels    9;  Gaps    3;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-------PGKE 53
              |||:  | |:::|| | |||       ||||||::  |:| : ||| ::         ||:|
Db          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65

Qy         54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
               | :  |:|| ||:||||| |  |:|:|| ||| |:|||   |||:|: || |||| | :
Db         66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125

Qy        114 GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
              |||: ||:|:||||||:||||||||||:|   | |  | |||: | :|||:  ||: ||
Db        126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQL 185

Qy        174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEKCHLGGRW 227
              |||||||| | | |||||   ||  | ||| | |||||||||:: |||  ||  |
Db        186 GLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240


RESULT 8
US-09-949-016-7232
; Sequence 7232, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7232
;   LENGTH: 241
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-7232

  Query Match             56.5%;  Score 735.5;  DB 4;  Length 241;
  Best Local Similarity   57.0%;  Pred. No. 3.1e-65;
  Matches  134;  Conservative   31;  Mismatches   61;  Indels    9;  Gaps    3;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-------PGKE 53
              |||:  | |:::|| | |||       ||||||::  |:| : ||| ::         ||:|
Db          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65

Qy         54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
               | :  |:|| ||:||||| |  |:|:|| ||| |:|||   |||:|: || |||| | :
Db         66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125

Qy        114 GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
              |||: ||:|:||||||:||||||||||:|   | |  | |||: | :|||:  ||: ||
Db        126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQL 185

Qy        174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEKCHLGGRW 227
              |||||||| | | |||||   ||  | ||| | |||||||||:: |||  ||  |
Db        186 GLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240


RESULT 9
US-08-911-423-6
; Sequence 6, Application US/08911423
; Patent No. 6111090
;  GENERAL INFORMATION:
;    APPLICANT:  Gorman, Daniel M.
;    APPLICANT:  Randall, Troy D.
;    APPLICANT:  Zlotnik, Albert
;    TITLE OF INVENTION:  MAMMALIAN CELL SURFACE ANTIGENS; RELATED
;    TITLE OF INVENTION:  REAGENTS
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/911,423
;      FILING DATE:  14-AUG-1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/023,419
;      FILING DATE:  16-AUG-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/027,901
;      FILING DATE:  07-OCT-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  DX0612K
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-852-9196
;      TELEFAX:  650-496-1200
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  228 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-911-423-6
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  Best Local Similarity   54.9%;  Pred. No. 5e-62;
  Matches  129;  Conservative   32;  Mismatches   58;  Indels   16;  Gaps    4;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-------PGKE 53
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Db          1 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 59

Qy         54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
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Qy        174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEKCHLGGRW 227
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RESULT 10
US-09-512-363-2
; Sequence 2, Application US/09512363
; Patent No. 6503184
; GENERAL INFORMATION:
;  APPLICANT: Ni, Jian
;  APPLICANT: Ruben, Steven M.
;  TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
;  TITLE OF INVENTION: TR11, TR11SV1, and TR11SV2
;  FILE REFERENCE: PF396
;  CURRENT APPLICATION NUMBER: US/09/512,363
;  CURRENT FILING DATE: 2000-02-23
;  EARLIER APPLICATION NUMBER: 60/063,212
;  EARLIER FILING DATE: 1997-10-21
;  EARLIER APPLICATION NUMBER: 09/176,200
;  EARLIER FILING DATE: 1998-10-21
;  EARLIER APPLICATION NUMBER: 60/121,648
;  EARLIER FILING DATE: 1999-02-24
;  EARLIER APPLICATION NUMBER: 60/134,172
;  EARLIER FILING DATE: 1999-05-13
;  EARLIER APPLICATION NUMBER: 60/144,076
;  EARLIER FILING DATE: 1999-07-16
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 234
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-512-363-2

  Query Match             54.0%;  Score 703;  DB 4;  Length 234;
  Best Local Similarity   54.9%;  Pred. No. 5.2e-62;
  Matches  129;  Conservative   32;  Mismatches   58;  Indels   16;  Gaps    4;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-------PGKE 53
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Db          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65

Qy         54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
               | :  |:|| ||:||||| |  |:|:|| ||| |:|||   |||:|: || |||| | :
Db         66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125

Qy        114 GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
              |||: ||:|:|||||||:|||||||||||:|   | |  | |||: | :|||:  ||: ||
Db        126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQL 185

Qy        174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEKCHLGGRW 227
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Db        186 GLHIWQLRK-------TQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 233


RESULT 11
US-09-176-200-2
; Sequence 2, Application US/09176200
; Patent No. 6509173
; GENERAL INFORMATION:
;  APPLICANT: Ni, Jian
;  APPLICANT: Ruben, Steven M.
;  TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
;  TITLE OF INVENTION: TR11, TR11SV1, and TR11SV2
;  FILE REFERENCE: PF396
;  CURRENT APPLICATION NUMBER: US/09/176,200
;  CURRENT FILING DATE: 1998-10-21
;  EARLIER APPLICATION NUMBER: 60/063,212
;  EARLIER FILING DATE: 1997-10-21
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 234
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-176-200-2

  Query Match             54.0%;  Score 703;  DB 4;  Length 234;
  Best Local Similarity   54.9%;  Pred. No. 5.2e-62;
  Matches  129;  Conservative   32;  Mismatches   58;  Indels   16;  Gaps    4;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-------PGKE 53
              |||:  | |:::|| | |||      ||||||::  |:| : ||| ::        ||:|
Db          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65

Qy         54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
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Qy        114 GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
              |||: ||:|:|||||||:|||||||||||:|   | |  | |||: | :|||:  ||: ||
Db        126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQL 185

Qy        174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEKCHLGGRW 227
              ||||||||:       ||   ||  | ||| | |||||||||:: |||  ||  |
Db        186 GLHIWQLRK-------TQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 233


RESULT 12
US-09-915-593-2
; Sequence 2, Application US/09915593
; Patent No. 6689607
; GENERAL INFORMATION:
;  APPLICANT: Ni, Jian
;  APPLICANT:  Ruben, Steven M.
;  TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
;  TITLE OF INVENTION:  TR11, TR11SV1, and TR11SV2
;  FILE REFERENCE: PF396P2
;  CURRENT APPLICATION NUMBER: US/09/915,593
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/221,577
;  PRIOR FILING DATE: 2000-07-28
;  PRIOR APPLICATION NUMBER: 09/512,363
;  PRIOR FILING DATE: 2000-02-23
;  PRIOR APPLICATION NUMBER: 60/144,076
;  PRIOR FILING DATE: 2000-07-16
;  PRIOR APPLICATION NUMBER: 60/134,172
;  PRIOR FILING DATE: 1999-05-13
;  PRIOR APPLICATION NUMBER: 60/121,648
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 09/176,200
;  PRIOR FILING DATE: 1998-10-21
;  PRIOR APPLICATION NUMBER: 60/063,212
;  PRIOR FILING DATE: 1997-10-21
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 234
;   TYPE: PRT
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;   ORGANISM: Homo sapiens
US-09-915-593-2

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  Best Local Similarity   54.9%;  Pred. No. 5.2e-62;
  Matches  129;  Conservative   32;  Mismatches   58;  Indels   16;  Gaps    4;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-------PGKE 53
              |||:  | |:::|| | |||      ||||||::  |:| : ||| ::        ||:|
Db          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65

Qy         54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
               | :  |:|| ||:|||| |  |:|:|| ||| |:|||   |||:|: || |||| | :
Db         66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125

Qy        114 GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
              |||: ||:|:||||||:||||||||||:|   | |  | |||: | :|||:  ||: ||
Db        126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQL 185

Qy        174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEKCHLGGRW 227
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Db        186 GLHIWQLRK-------TQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 233


RESULT 13
US-09-512-363-6
; Sequence 6, Application US/09512363
; Patent No. 6503184
; GENERAL INFORMATION:
;  APPLICANT: Ni, Jian
;  APPLICANT: Ruben, Steven M.
;  TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
;  TITLE OF INVENTION: TR11, TR11SV1, and TR11SV2
;  FILE REFERENCE: PF396
;  CURRENT APPLICATION NUMBER: US/09/512,363
;  CURRENT FILING DATE: 2000-02-23
;  EARLIER APPLICATION NUMBER: 60/063,212
;  EARLIER FILING DATE: 1997-10-21
;  EARLIER APPLICATION NUMBER: 09/176,200
;  EARLIER FILING DATE: 1998-10-21
;  EARLIER APPLICATION NUMBER: 60/121,648
;  EARLIER FILING DATE: 1999-02-24
;  EARLIER APPLICATION NUMBER: 60/134,172
;  EARLIER FILING DATE: 1999-05-13
;  EARLIER APPLICATION NUMBER: 60/144,076
;  EARLIER FILING DATE: 1999-07-16
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-512-363-6

  Query Match             53.6%;  Score 697;  DB 4;  Length 240;
  Best Local Similarity   52.2%;  Pred. No. 2.1e-61;
  Matches  129;  Conservative   32;  Mismatches   58;  Indels   28;  Gaps    4;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLY------------ 48
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Qy         49 -------APGKEDCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCV 101
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Qy        162 AACIFFLTTVQLGLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEK 220
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; Sequence 6, Application US/09176200
; Patent No. 6509173
; GENERAL INFORMATION:
;  APPLICANT: Ni, Jian
;  APPLICANT: Ruben, Steven M.
;  TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
;  TITLE OF INVENTION: TR11, TR11SV1, and TR11SV2
;  FILE REFERENCE: PF396
;  CURRENT APPLICATION NUMBER: US/09/176,200
;  CURRENT FILING DATE: 1998-10-21
;  EARLIER APPLICATION NUMBER: 60/063,212
;  EARLIER FILING DATE: 1997-10-21
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-176-200-6

  Query Match             53.6%;  Score 697;  DB 4;  Length 240;
  Best Local Similarity   52.2%;  Pred. No. 2.1e-61;
  Matches  129;  Conservative   32;  Mismatches   58;  Indels   28;  Gaps    4;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLY------------ 48
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Db          1 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPAQL 59

Qy         49 -------APGKEDCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCV 101
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Db        233 GRLGDLW 239


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; Sequence 6, Application US/09915593
; Patent No. 6689607
; GENERAL INFORMATION:
;  APPLICANT: Ni, Jian
;  APPLICANT:  Ruben, Steven M.
;  TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
;  TITLE OF INVENTION:  TR11, TR11SV1, and TR11SV2
;  FILE REFERENCE: PF396P2
;  CURRENT APPLICATION NUMBER: US/09/915,593
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/221,577
;  PRIOR FILING DATE: 2000-07-28
;  PRIOR APPLICATION NUMBER: 09/512,363
;  PRIOR FILING DATE: 2000-02-23
;  PRIOR APPLICATION NUMBER: 60/144,076
;  PRIOR FILING DATE: 2000-07-16
;  PRIOR APPLICATION NUMBER: 60/134,172
;  PRIOR FILING DATE: 1999-05-13
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;  PRIOR APPLICATION NUMBER: 60/121,648
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 09/176,200
;  PRIOR FILING DATE: 1998-10-21
;  PRIOR APPLICATION NUMBER: 60/063,212
;  PRIOR FILING DATE: 1997-10-21
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-915-593-6

  Query Match             53.6%;  Score 697;  DB 4;  Length 240;
  Best Local Similarity   52.2%;  Pred. No. 2.1e-61;
  Matches  129;  Conservative   32;  Mismatches   58;  Indels   28;  Gaps    4;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLY------------ 48
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Db          1 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPAQL 59

Qy         49 -------APGKEDCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCV 101
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Db         60 LGGWPVSCPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCI 119

Qy        102 ACAMGTFSAGRDGHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVM 161
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Qy        162 AACIFFLTTVQLGLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEK 220
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Db        180 AACVLLLTSAQLGLHIWQLRK-------TQLLLEVPPSTEDARSCQFPEEERGERSAEEK 232

Qy        221 CHLGGRW 227
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Db        233 GRLGDLW 239


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GenCore version 5.1.6

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(without alignments)
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Title: US-09-545-998B-2
Perfect score: 1301
Sequence: 1 MGAWAMLYGVSMLCVLDLGQ.....PEEERGEQTEEKCHLGGRWP 228

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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SUMMARIES

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3	1301	100.0	228	14	US-10-283-105-7	Sequence 7, Appli
4	1301	100.0	228	14	US-10-277-966-7	Sequence 7, Appli
5	1301	100.0	228	17	US-10-959-537-24	Sequence 24, Appl
6	735.5	56.5	240	16	US-10-783-528-75	Sequence 75, Appl
7	735.5	56.5	241	9	US-09-915-593-28	Sequence 28, Appl
8	735.5	56.5	241	13	US-10-116-378-3	Sequence 3, Appli
9	735.5	56.5	241	14	US-10-283-105-28	Sequence 28, Appl
10	735.5	56.5	241	14	US-10-277-966-28	Sequence 28, Appl
11	735.5	56.5	241	15	US-10-295-027-1284	Sequence 1284, Ap
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13	735.5	56.5	241	20	US-11-032-294-3	Sequence 3, Appli
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23	630.5	48.5	241	14	US-10-277-966-4	Sequence 4, Appli
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33	228.5	17.6	255	13	US-10-027-199-2	Sequence 2, Appli
34	228.5	17.6	255	14	US-10-170-997-2	Sequence 2, Appli
35	228.5	17.6	255	14	US-10-186-643-11	Sequence 11, Appl
36	228.5	17.6	255	14	US-10-207-655-160	Sequence 160, App
37	228.5	17.6	255	15	US-10-418-242-13	Sequence 13, Appl
38	228.5	17.6	255	16	US-10-646-308-18	Sequence 18, Appl
39	228.5	17.6	255	16	US-10-755-889-174	Sequence 174, App
40	228.5	17.6	255	16	US-10-748-112-15	Sequence 15, Appl
41	228.5	17.6	255	16	US-10-723-860-588	Sequence 588, App
42	228.5	17.6	255	17	US-10-491-997-32	Sequence 32, Appl
43	228.5	17.6	255	17	US-10-981-352-2	Sequence 2, Appli
44	222.5	17.1	219	9	US-09-739-394-2	Sequence 2, Appli
45	222.5	17.1	219	13	US-10-097-330-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-915-593-7
; Sequence 7, Application US/09915593
; Patent No. US20020098525A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
; TITLE OF INVENTION: TR11, TR11SV1, and TR11SV2
; FILE REFERENCE: PF396P2
; CURRENT APPLICATION NUMBER: US/09/915,593
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/221,577
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/512,363
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/144,076
; PRIOR FILING DATE: 2000-07-16
; PRIOR APPLICATION NUMBER: 60/134,172
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/121,648
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 09/176,200
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/063,212
; PRIOR FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-915-593-7

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  Query Match             100.0%;  Score 1301;  DB 9;  Length 228;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-114;
  Matches  228;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60
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Db          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60

Qy         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120
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Qy        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180

Qy        181 RRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP 228
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Db        181 RRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP 228


RESULT 2
US-10-116-378-24
; Sequence 24, Application US/10116378
; Publication No. US20020150993A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi J.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Gurney, Austin
;  APPLICANT:  Marsters, Scot A.
;  APPLICANT:  Pitti, Robert M.
;  APPLICANT:  Wood, William
;  TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND
;  TITLE OF INVENTION:  NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P1206R1
;  CURRENT APPLICATION NUMBER: US/10/116,378
;  CURRENT FILING DATE:  2002-04-04
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
;  NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 24
;   LENGTH: 228
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-116-378-24

  Query Match             100.0%;  Score 1301;  DB 13;  Length 228;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-114;
  Matches  228;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60

Qy         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120

Qy        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180

Qy        181 RRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP 228
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Db        181 RRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP 228


RESULT 3
US-10-283-105-7
; Sequence 7, Application US/10283105
; Publication No. US20030138426A1
; GENERAL INFORMATION:
;  APPLICANT: Ni, Jian
;  APPLICANT:  Ruben, Steven M
;  TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,
;  TITLE OF INVENTION:  TR11Sv22
;  FILE REFERENCE: PF396P3
;  CURRENT APPLICATION NUMBER: US/10/283,105
;  CURRENT FILING DATE:  2002-10-30
;  PRIOR APPLICATION NUMBER: 60/330,757
;  PRIOR FILING DATE: 2001-10-30
;  PRIOR APPLICATION NUMBER: 09/915,593
;  PRIOR FILING DATE: 2001-07-27
;  PRIOR APPLICATION NUMBER: 60/221,577
;  PRIOR FILING DATE: 2000-07-28
;  PRIOR APPLICATION NUMBER: 09/512,363
;  PRIOR FILING DATE: 2000-02-23
;  PRIOR APPLICATION NUMBER: 60/144,076
;  PRIOR FILING DATE: 1999-07-16
;  PRIOR APPLICATION NUMBER: 60/134,172
;  PRIOR FILING DATE: 1999-05-13
;  PRIOR APPLICATION NUMBER: 60/121,648
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 09/176,200
;  PRIOR FILING DATE: 1998-10-21
;  PRIOR APPLICATION NUMBER: 60/063,212
;  PRIOR FILING DATE: 1997-10-21
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 228
;   TYPE: PRT
;   ORGANISM: mus musculus
US-10-283-105-7

  Query Match             100.0%;  Score 1301;  DB 14;  Length 228;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-114;
  Matches  228;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60

Qy         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120

Qy        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180

Qy        181 RRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP 228
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP 228


RESULT 4
US-10-277-966-7
; Sequence 7, Application US/10277966
; Publication No. US20030153499A1
; GENERAL INFORMATION:
;  APPLICANT: Ni, Jian
;  APPLICANT:  Ruben, Steven
;  TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,
;  TITLE OF INVENTION:  TR11SV2
;  FILE REFERENCE: PF396P1D1
;  CURRENT APPLICATION NUMBER: US/10/277,966
;  CURRENT FILING DATE:  2002-10-23
;  PRIOR APPLICATION NUMBER: 09/512,363
;  PRIOR FILING DATE: 2000-02-23
;  PRIOR APPLICATION NUMBER: 60/121,648
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 60/134,172
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;  PRIOR FILING DATE: 1999-05-13
;  PRIOR APPLICATION NUMBER: 60/144,076
;  PRIOR FILING DATE: 1999-07-16
;  PRIOR APPLICATION NUMBER: 09/176,200
;  PRIOR FILING DATE: 1998-10-21
;  PRIOR APPLICATION NUMBER: 60/063,212
;  PRIOR FILING DATE: 1997-10-21
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 228
;   TYPE: PRT
;   ORGANISM: mouse
US-10-277-966-7

  Query Match            100.0%;  Score 1301;  DB 14;  Length 228;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-114;
  Matches  228;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60
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Db          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60

Qy         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120

Qy        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180

Qy        181 RRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP 228
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Db        181 RRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP 228


RESULT 5
US-10-959-537-24
; Sequence 24, Application US/10959537
; Publication No. US20050069983A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi J.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Gurney, Austin
;  APPLICANT:  Marsters, Scot A.
;  APPLICANT:  Pitti, Robert M.
;  APPLICANT:  Wood, William
;  TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P1206R1
;  CURRENT APPLICATION NUMBER: US/10/959,537
;  CURRENT FILING DATE:  2004-10-06
;  PRIOR APPLICATION NUMBER: US/09/247,225
;  PRIOR FILING DATE: 1999-02-09
;  PRIOR APPLICATION NUMBER: US 60/074,087
;  PRIOR FILING DATE: 1998-02-09
;  NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 24
;   LENGTH: 228
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-959-537-24

  Query Match            100.0%;  Score 1301;  DB 17;  Length 228;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-114;
  Matches  228;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60

Qy         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120

Qy        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180

Qy        181 RRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP 228
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Db        181 RRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP 228


RESULT 6
US-10-783-528-75
; Sequence 75, Application US/10783528
; Publication No. US20040219579A1
; GENERAL INFORMATION:
;  APPLICANT: Aziz, Natasha
;  APPLICANT:  Gish, Kurt
;  APPLICANT:  Wilson, Keith
;  APPLICANT:  Zlotnik, Albert
;  TITLE OF INVENTION: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND
;  FILE REFERENCE: 05882.0191.NPUS01
;  CURRENT APPLICATION NUMBER: US/10/783,528
;  CURRENT FILING DATE:  2004-02-19
;  NUMBER OF SEQ ID NOS: 116
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 75
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-783-528-75

  Query Match            56.5%;  Score 735.5;  DB 16;  Length 240;
  Best Local Similarity  57.0%;  Pred. No. 5e-61;
  Matches  134;  Conservative   31;  Mismatches   61;  Indels    9;  Gaps    3;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-------PGKE 53
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Db          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65

Qy         54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
               | :  |:|| ||:|||| |  |:|:|| ||| |:|||   |||:|: || |||| | :
Db         66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125

Qy        114 GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
              |||: ||:|:||||||:||||||||||:|    | |  | |||: | :|||:  ||: ||
Db        126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQL 185

Qy        174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEKCHLGGRW 227
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Db        186 GLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240


RESULT 7
US-09-915-593-28
; Sequence 28, Application US/09915593
; Patent No. US20020098525A1
; GENERAL INFORMATION:
;  APPLICANT: Ni, Jian
;  APPLICANT:  Ruben, Steven M.
;  TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
;  TITLE OF INVENTION:  TR11, TR11SV1, and TR11SV2
;  FILE REFERENCE: PF396P2
;  CURRENT APPLICATION NUMBER: US/09/915,593
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/221,577
;  PRIOR FILING DATE: 2000-07-28
;  PRIOR APPLICATION NUMBER: 09/512,363
;  PRIOR FILING DATE: 2000-02-23
;  PRIOR APPLICATION NUMBER: 60/144,076
;  PRIOR FILING DATE: 2000-07-16
;  PRIOR APPLICATION NUMBER: 60/134,172
;  PRIOR FILING DATE: 1999-05-13
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;  PRIOR APPLICATION NUMBER: 60/121,648
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 09/176,200
;  PRIOR FILING DATE: 1998-10-21
;  PRIOR APPLICATION NUMBER: 60/063,212
;  PRIOR FILING DATE: 1997-10-21
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
;   LENGTH: 241
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-915-593-28

  Query Match             56.5%;  Score 735.5;  DB 9;  Length 241;
  Best Local Similarity   57.0%;  Pred. No. 5e-61;
  Matches  134;  Conservative   31;  Mismatches   61;  Indels    9;  Gaps    3;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-------PGKE 53
              |||:  | |:::|| | |||      ||||||::  |:| : ||| ::        ||:|
Db          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65

Qy         54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
                | :  |:|| ||:||||| |  |:|:|| ||| |:|||   |||:|: || |||| | :
Db         66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125

Qy        114 GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
              |||: ||:|:||||||:||||||||||:|   | |  | |||: | :|||:  ||: ||
Db        126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQL 185

Qy        174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEKCHLGGRW 227
              |||||||| | | |||||   ||  | ||| | |||||||||:: |||  ||  |
Db        186 GLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240


RESULT 8
US-10-116-378-3
; Sequence 3, Application US/10116378
; Publication No. US20020150993A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi J.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Gurney, Austin
;  APPLICANT:  Marsters, Scot A.
;  APPLICANT:  Pitti, Robert M.
;  APPLICANT:  Wood, William
;  TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND
;  TITLE OF INVENTION:  NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P1206R1
;  CURRENT APPLICATION NUMBER: US/10/116,378
;  CURRENT FILING DATE:  2002-04-04
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
;  NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 3
;   LENGTH: 241
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-116-378-3

  Query Match             56.5%;  Score 735.5;  DB 13;  Length 241;
  Best Local Similarity   57.0%;  Pred. No. 5e-61;
  Matches  134;  Conservative   31;  Mismatches   61;  Indels    9;  Gaps    3;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-------PGKE 53
              |||:  | |:::|| | |||      ||||||::  |:| : ||| ::        ||:|
Db          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65

Qy         54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
                | :  |:|| ||:||||| |  |:|:|| ||| |:|||   |||:|: || |||| | :
Db         66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125

Qy        114 GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
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Db        126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQL 185

Qy        174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEKCHLGGRW 227
              |||||||| | | |||||   ||  | ||| | |||||||||:: |||  ||  |
Db        186 GLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240


RESULT 9
US-10-283-105-28
; Sequence 28, Application US/10283105
; Publication No. US20030138426A1
; GENERAL INFORMATION:
;  APPLICANT: Ni, Jian
;  APPLICANT:  Ruben, Steven M
;  TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,
;  TITLE OF INVENTION:  TR11Sv22
;  FILE REFERENCE: PF396P3
;  CURRENT APPLICATION NUMBER: US/10/283,105
;  CURRENT FILING DATE:  2002-10-30
;  PRIOR APPLICATION NUMBER: 60/330,757
;  PRIOR FILING DATE: 2001-10-30
;  PRIOR APPLICATION NUMBER: 09/915,593
;  PRIOR FILING DATE: 2001-07-27
;  PRIOR APPLICATION NUMBER: 60/221,577
;  PRIOR FILING DATE: 2000-07-28
;  PRIOR APPLICATION NUMBER: 09/512,363
;  PRIOR FILING DATE: 2000-02-23
;  PRIOR APPLICATION NUMBER: 60/144,076
;  PRIOR FILING DATE: 1999-07-16
;  PRIOR APPLICATION NUMBER: 60/134,172
;  PRIOR FILING DATE: 1999-05-13
;  PRIOR APPLICATION NUMBER: 60/121,648
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 09/176,200
;  PRIOR FILING DATE: 1998-10-21
;  PRIOR APPLICATION NUMBER: 60/063,212
;  PRIOR FILING DATE: 1997-10-21
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
;   LENGTH: 241
;   TYPE: PRT
;   ORGANISM: human
US-10-283-105-28

  Query Match             56.5%;  Score 735.5;  DB 14;  Length 241;
  Best Local Similarity   57.0%;  Pred. No. 5e-61;
  Matches  134;  Conservative   31;  Mismatches   61;  Indels    9;  Gaps    3;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-------PGKE 53
              |||:  | |:::|| | |||      ||||||::  |:| : ||| ::        ||:|
Db          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65

Qy         54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
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Qy        114 GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
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Db        126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQL 185

Qy        174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEKCHLGGRW 227
              |||||||| | | |||||   ||  | ||| | |||||||||:: |||  ||  |
Db        186 GLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240


RESULT 10
US-10-277-966-28
; Sequence 28, Application US/10277966
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; Publication No. US20030153499A1
; GENERAL INFORMATION:
;  APPLICANT: Ni, Jian
;  APPLICANT:  Ruben, Steven
;  TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,
;  TITLE OF INVENTION:  TR11SV2
;  FILE REFERENCE: PF396P1D1
;  CURRENT APPLICATION NUMBER: US/10/277,966
;  CURRENT FILING DATE:  2002-10-23
;  PRIOR APPLICATION NUMBER: 09/512,363
;  PRIOR FILING DATE: 2000-02-23
;  PRIOR APPLICATION NUMBER: 60/121,648
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 60/134,172
;  PRIOR FILING DATE: 1999-05-13
;  PRIOR APPLICATION NUMBER: 60/144,076
;  PRIOR FILING DATE: 1999-07-16
;  PRIOR APPLICATION NUMBER: 09/176,200
;  PRIOR FILING DATE: 1998-10-21
;  PRIOR APPLICATION NUMBER: 60/063,212
;  PRIOR FILING DATE: 1997-10-21
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
;   LENGTH: 241
;   TYPE: PRT
;   ORGANISM: human
US-10-277-966-28

  Query Match             56.5%;  Score 735.5;  DB 14;  Length 241;
  Best Local Similarity   57.0%;  Pred. No. 5e-61;
  Matches  134;  Conservative   31;  Mismatches   61;  Indels    9;  Gaps    3;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-------PGKE 53
              |||:  | |:::|| | |||      ||||||::  |:| : ||| ::        ||:|
Db          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65

Qy         54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
               | :  |:|| ||:|||| |  |:|:|| ||| |:||   |||:|: || |||| | :
Db         66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125

Qy        114 GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
              |||: ||:|:|||||:||||||||||:|   | |  | |||: | :|||:  ||: ||
Db        126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQL 185

Qy        174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEKCHLGGRW 227
              |||||||| | | |||||    ||  | ||| | |||||||||:: |||  ||  |
Db        186 GLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240


RESULT 11
US-10-295-027-1284
; Sequence 1284, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
;  APPLICANT: Afar, Daniel
;  APPLICANT:  Aziz, Natasha
;  APPLICANT:  Ginsberg, Wendy M.
;  APPLICANT:  Gish, Kurt C.
;  APPLICANT:  Glynne, Richard
;  APPLICANT:  Hevezi, Peter A.
;  APPLICANT:  Mack, David H.
;  APPLICANT:  Murray, Richard
;  APPLICANT:  Watson, Susan R.
;  APPLICANT:  Eos Biotechnology, Inc.
;  TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
;  TITLE OF INVENTION:  Methods of Screening for Modulators of Cancer
;  FILE REFERENCE: 018501-012500US
;  CURRENT APPLICATION NUMBER: US/10/295,027
;  CURRENT FILING DATE:  2002-11-13
;  PRIOR APPLICATION NUMBER: US 09/663,733
;  PRIOR FILING DATE: 2000-09-15
;  PRIOR APPLICATION NUMBER: US 60/350,666
;  PRIOR FILING DATE: 2001-11-13
;  PRIOR APPLICATION NUMBER: US 60/335,394
;  PRIOR FILING DATE: 2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/332,464
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: US 60/334,393
;  PRIOR FILING DATE: 2001-11-29
;  PRIOR APPLICATION NUMBER: US 60/340,376
;  PRIOR FILING DATE: 2001-12-14
;  PRIOR APPLICATION NUMBER: US 60/347,211
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: US 60/347,349
;  PRIOR FILING DATE: 2002-01-10
;  PRIOR APPLICATION NUMBER: US 60/355,250
;  PRIOR FILING DATE: 2002-02-08
;  PRIOR APPLICATION NUMBER: US 60/356,714
;  PRIOR FILING DATE: 2002-02-13
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1386
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1284
;   LENGTH: 241
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-295-027-1284

  Query Match             56.5%;  Score 735.5;  DB 15;  Length 241;
  Best Local Similarity   57.0%;  Pred. No. 5e-61;
  Matches  134;  Conservative   31;  Mismatches   61;  Indels    9;  Gaps    3;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-------PGKE 53
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Db          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65

Qy         54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
               | :  |:|| ||:|||| |  |:|:|| ||| |:||   |||:|: || |||| | :
Db         66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125

Qy        114 GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
              |||: ||:|:|||||:||||||||||:|   | |  | |||: | :|||:  ||: ||
Db        126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQL 185

Qy        174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEKCHLGGRW 227
              |||||||| | | |||||    ||  | ||| | |||||||||:: |||  ||  |
Db        186 GLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240


RESULT 12
US-10-959-537-3
; Sequence 3, Application US/10959537
; Publication No. US20050069983A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi J.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Gurney, Austin
;  APPLICANT:  Marsters, Scot A.
;  APPLICANT:  Pitti, Robert M.
;  APPLICANT:  Wood, William
;  TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P1206R1
;  CURRENT APPLICATION NUMBER: US/10/959,537
;  CURRENT FILING DATE:  2004-10-06
;  PRIOR APPLICATION NUMBER: US/09/247,225
;  PRIOR FILING DATE: 1999-02-09
;  PRIOR APPLICATION NUMBER: US 60/074,087
;  PRIOR FILING DATE: 1998-02-09
;  NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 3
;   LENGTH: 241
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-959-537-3
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  Query Match             56.5%;  Score 735.5;  DB 17;  Length 241;
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  Matches  134;  Conservative   31;  Mismatches   61;  Indels    9;  Gaps    3;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-------PGKE 53
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Db          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65

Qy         54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
               | :  |:|| ||:|||||  |  |:|:|| ||| |:|||   |||:|: || |||| | :
Db         66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125

Qy        114 GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
              |||: ||:|:|||||:||||||||||:|   | |  | |||: | :|||:  ||: ||
Db        126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQL 185

Qy        174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEKCHLGGRW 227
              |||||||| | | |||||   ||  | ||| | |||||||||:: |||  ||  |
Db        186 GLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240


RESULT 13
US-11-032-294-3
; Sequence 3, Application US/11032294
; Publication No. US20050202008A1
; GENERAL INFORMATION:
;  APPLICANT: P. Mickey Williams
;  APPLICANT:  Mary E. Gerritsen
;  TITLE OF INVENTION: PROMOTION OR INHIBITION OF ANGIOGENESIS AND
;  TITLE OF INVENTION:  CARDIOVASCULARIZATION BY TUMOR NECROSIS FACTOR
;  TITLE OF INVENTION:  LIGAND/RECEPTOR HOMOLOGS
;  FILE REFERENCE: P1765R1
;  CURRENT APPLICATION NUMBER: US/11/032,294
;  CURRENT FILING DATE:  2005-01-10
;  PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/613,972
;  PRIOR FILING DATE: CURRENT FILING DATE:  2000-07-11
;  PRIOR APPLICATION NUMBER: US 60/143,304
;  PRIOR FILING DATE: 1999-07-12
;  NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 3
;   LENGTH: 241
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-032-294-3

  Query Match             56.5%;  Score 735.5;  DB 20;  Length 241;
  Best Local Similarity   57.0%;  Pred. No. 5e-61;
  Matches  134;  Conservative   31;  Mismatches   61;  Indels    9;  Gaps    3;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-------PGKE 53
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Db          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65

Qy         54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
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Qy        114 GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
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Qy        174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEKCHLGGRW 227
              |||||||| | | |||||   ||  | ||| | |||||||||:: |||  ||  |
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RESULT 14
US-09-915-593-2
; Sequence 2, Application US/09915593
; Patent No. US20020098525A1
; GENERAL INFORMATION:
;  APPLICANT: Ni, Jian
;  APPLICANT:  Ruben, Steven M.
;  TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
;  TITLE OF INVENTION:  TR11, TR11SV1, and TR11SV2
;  FILE REFERENCE: PF396P2
;  CURRENT APPLICATION NUMBER: US/09/915,593
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/221,577
;  PRIOR FILING DATE: 2000-07-28
;  PRIOR APPLICATION NUMBER: 09/512,363
;  PRIOR FILING DATE: 2000-02-23
;  PRIOR APPLICATION NUMBER: 60/144,076
;  PRIOR FILING DATE: 2000-07-16
;  PRIOR APPLICATION NUMBER: 60/134,172
;  PRIOR FILING DATE: 1999-05-13
;  PRIOR APPLICATION NUMBER: 60/121,648
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 09/176,200
;  PRIOR FILING DATE: 1998-10-21
;  PRIOR APPLICATION NUMBER: 60/063,212
;  PRIOR FILING DATE: 1997-10-21
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 234
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-915-593-2

  Query Match             54.0%;  Score 703;  DB 9;  Length 234;
  Best Local Similarity   54.9%;  Pred. No. 5.6e-58;
  Matches  129;  Conservative   32;  Mismatches   58;  Indels   16;  Gaps    4;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-------PGKE 53
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Db          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65

Qy         54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
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Db         66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125

Qy        114 GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
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Db        126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQL 185

Qy        174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEKCHLGGRW 227
              |||||||:        ||   ||  | ||| | |||||||||:: |||  ||  |
Db        186 GLHIWQLRK-------TQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 233


RESULT 15
US-10-283-105-2
; Sequence 2, Application US/10283105
; Publication No. US20030138426A1
; GENERAL INFORMATION:
;  APPLICANT: Ni, Jian
;  APPLICANT:  Ruben, Steven M
;  TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,
;  TITLE OF INVENTION:  TR11Sv22
;  FILE REFERENCE: PF396P3
;  CURRENT APPLICATION NUMBER: US/10/283,105
;  CURRENT FILING DATE:  2002-10-30
;  PRIOR APPLICATION NUMBER: 60/330,757
;  PRIOR FILING DATE: 2001-10-30
;  PRIOR APPLICATION NUMBER: 09/915,593
;  PRIOR FILING DATE: 2001-07-27
;  PRIOR APPLICATION NUMBER: 60/221,577
;  PRIOR FILING DATE: 2000-07-28
;  PRIOR APPLICATION NUMBER: 09/512,363
;  PRIOR FILING DATE: 2000-02-23
;  PRIOR APPLICATION NUMBER: 60/144,076
;  PRIOR FILING DATE: 1999-07-16
;  PRIOR APPLICATION NUMBER: 60/134,172
;  PRIOR FILING DATE: 1999-05-13
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;  PRIOR APPLICATION NUMBER: 60/121,648
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 09/176,200
;  PRIOR FILING DATE: 1998-10-21
;  PRIOR APPLICATION NUMBER: 60/063,212
;  PRIOR FILING DATE: 1997-10-21
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 234
;   TYPE: PRT
;   ORGANISM: human
US-10-283-105-2

  Query Match             54.0%;  Score 703;  DB 14;  Length 234;
  Best Local Similarity   54.9%;  Pred. No. 5.6e-58;
  Matches  129;  Conservative   32;  Mismatches   58;  Indels   16;  Gaps    4;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-------PGKE 53
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Db          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65

Qy         54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
               | :  |:|| ||:|||||  |  |:|:|| ||| |:|||   |||:|: || |||| | :
Db         66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125

Qy        114 GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
              |||: ||:|:|||||||:||||||||||:|   | |  | |||: | :|||:  ||: ||
Db        126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQL 185

Qy        174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEEERGEQT-EEKCHLGGRW 227
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Job time : 111.382 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 26, 2005, 15:38:30 ; Search time 24.307 Seconds
(without alignments)
902.513 Million cell updates/sec

Title: US-09-545-998B-2
Perfect score: 1301
Sequence: 1 MGAWAMLYGVSMLCVLDLGQ.....PEEERGEQTEEKCHLGGRWP 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	228.5	17.6	255	2	I38426	lymphocyte activat
2	203.5	15.6	256	2	B32393	T-cell antigen 4-1
3	134	10.3	272	2	I48700	gene ox40 protein
4	126.5	9.7	271	2	S12783	OX40 antigen precu
5	125.5	9.6	250	1	A49053	CD27 antigen precu
6	122	9.4	277	2	I37552	OX40 homolog - hum
7	119	9.1	1113	2	JE0315	low-density lipopr
8	118.5	9.1	277	2	A60771	B-cell activation
9	115	8.8	435	2	I54182	tumor necrosis fac
10	107.5	8.3	459	2	I48854	gene murine tumour
11	106.5	8.2	474	2	B38634	tumor necrosis fac
12	104.5	8.0	305	2	A46476	B cell-associated
13	102.5	7.9	461	1	A35356	tumor necrosis fac
14	102.5	7.9	1260	1	TVRTNU	protein-tyrosine k
15	102.5	7.9	4543	1	A53102	alpha-2-macroglobu
16	100.5	7.7	1254	2	I48161	p-185 precursor -
17	100.5	7.7	2321	2	S78549	notch3 protein - h
18	100	7.7	260	1	A46517	CD27 antigen precu
19	99.5	7.6	651	2	JC7705	death receptor-6 -
20	99.5	7.6	1797	2	A55677	laminin beta-2 cha
21	99	7.6	655	2	JC7850	disintegrin and me
22	99	7.6	1964	2	T09059	notch4 - mouse
23	98	7.5	1251	2	A57293	latent transformin
24	95.5	7.3	918	2	JC4361	scavenger receptor
25	95	7.3	344	1	A27701	follistatin precur
26	95	7.3	344	2	A32141	follistatin 1 prec
27	95	7.3	344	2	I45894	follistatin - bovi
28	95	7.3	3635	2	T10053	laminin alpha 5 ch
29	94.5	7.3	329	2	A48805	insulin-like growt
30	93.5	7.2	1101	2	T16840	hypothetical prote
31	93.5	7.2	4545	1	S25111	alpha-2-macroglobu
32	93	7.1	227	1	LNRZ	lectin precursor -
33	93	7.1	337	2	I47079	follistatin - shee
34	93	7.1	343	2	S55369	follistatin - chic
35	93	7.1	1252	2	S36016	oocyst wall protei
36	93	7.1	1371	2	A33837	insulin-like growt
37	93	7.1	4391	2	A38096	perlecan precursor
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39	92	7.1	343	2	S45321	follistatin - mous
40	92	7.1	3507	2	T34513	hypothetical prote
41	91	7.0	1408	2	S16148	gene serrate prote
42	90.5	7.0	1034	2	JC5598	mucin - rat
43	90.5	7.0	2318	2	S45306	notch 3 protein -
44	89	6.8	768	2	I53821	P-selectin - rat
45	88.5	6.8	1217	1	EGMSMG	epidermal growth f

ALIGNMENTS

RESULT 1
I38426
lymphocyte activation-induced receptor ILA precursor - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I38426; JT0752
R;Alderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.; Rc
Eur. J. Immunol. 24, 2219-2227, 1994
A;Title: Molecular and biological characterization of human 4-1BB and its ligand.
A;Reference number: I38426; MUID:94374434; PMID:8088337
A;Accession: I38426
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-255 <RES>
A;Cross-references: UNIPROT:Q07011; EMBL:U03397; NID:g571320; PIDN:AAA53133.1; PID:g5713
R;Schwarz, H.; Tuckwell, J.; Lotz, M.
Gene 134, 295-298, 1993
A;Title: A receptor induced by lymphocyte activation (ILA): a new member of the human ne
A;Reference number: JT0752; MUID:94085794; PMID:8262389
A;Accession: JT0752
A;Molecule type: mRNA
A;Residues: 1-106,'R',108-255 <SCH>
C;Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-necro
C;Comment: This receptor recognizes soluble, cell-surface bound or extracellular matrix
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-255/Product: lymphocyte activation-induced receptor ILA #status predicted <MAT>
F;187-213/Domain: transmembrane #status predicted <TMM>
F;138,149/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;234,235/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predicte
F;242/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 17.6%; Score 228.5; DB 2; Length 255;
Best Local Similarity 27.2%; Pred. No. 7.5e-12;
Matches 68; Conservative 30; Mismatches 97; Indels 55; Gaps 10;

```
Qy          11 SMLCVLDLGQPSVVEEP------------------GCGPGKVQNGSGNNT-----RCCS 46
               ::| ||:  :   :::|                  | |    :  | |     :|
Db          11 TLLLVLNFERTRSLQDPCSNCPAGTFCDNNRNQICSPCPPNSFSSAGGQRTCDICRQCKG 70

Qy          47 LYAPGKE--DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACA 104
               ::   ||       | | || :||    | :|:   |: || :  :|      | |
Db          71 VFRTRKECSSTSNAECDC-TPGFHCLGAGCSMCEQ-DCKQGQELTKKG-------CKDCC 121

Qy         105 MGTFSAGRDGHCRLWTNCSQFGFLTMFPGNKTHNAVCIPE------------PLPTEQY 151
               |||:  : | || |||||  |   :  | |  : || |               | |  :
Db         122 FGTFNDQKRGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGASSVTPPAPAREP 181

Qy         152 GHLTVIF-----LVMAACIFFLTTVQLGLHIWQLRRQHMCPRETQPFAE-VQLS-AEDAC 204
               ||   |     |  | :| | : |  : :  |: :     |||   || :  || |
Db         182 GHSPQIISFFLALTSTALLFLLFFLTLRFSVVKRGRKKLLYIFKQPFMRPVQTTQEEDGC 241
```

```
Qy        205 SFQFPEEERG 214
              | :||||| |
Db        242 SCRFPEEEEG 251
```

RESULT 2
B32393
T-cell antigen 4-1BB precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: B32393; I48879
R;Kwon, B.S.; Weissman, S.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989
A;Title: cDNA sequence of two inducible T-cell genes.
A;Reference number: A32393; MUID:89184547; PMID:2784565
A;Accession: B32393
A;Molecule type: mRNA
A;Residues: 1-256 <KWO>
A;Cross-references: UNIPROT:P20334; GB:J04492; NID:g201121; PIDN:AAA40167.1; PID:g201122
R;Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.T.
J. Immunol. 152, 2256-2262, 1994
A;Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1BB.
A;Reference number: I48879; MUID:94179805; PMID:8133039
A;Accession: I48879
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-256 <RES>
A;Cross-references: EMBL:U02567; NID:g1117783; PIDN:AAA93113.1; PID:g409178
C;Genetics:
A;Introns: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: transmembrane protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-256/Product: 4-1BB protein #status predicted <MAT>

  Query Match 15.6%; Score 203.5; DB 2; Length 256;
  Best Local Similarity 29.8%; Pred. No. 9e-10;
  Matches 64; Conservative 26; Mismatches 84; Indels 41; Gaps 10;

```
Qy         22 SVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCP---KERCICVTPEYHCGDPQCKICK 78
              |:  :| |           | | |: |   |: |       | |:   :|| |||  |:
Db         54 SIGGQPNC----------NICRVCAGYFRFKKFCSSTHNAECECI-EGFHCLGPQCTRCE 102

Qy         79 HYPCQPGQRVESQGDIVFGFRCVACAMGTFS-AGRDGHCRLWTNCSQFGFLTMFPGNKTH 137
                |:||| :  ||       |  |::|||:     | || |||||  |   :  |
Db        103 K-DCRPGQELTKQG-------CKTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEK 154

Qy        138 NAVCIP-----EPLPTEQY-------GH----LTVIFLVMAACIFFLTTVQLGLHIWQLR 181
              : || |      |  |             ||    ||:   : :| :  |  : |   : :
Db        155 DVVCGPPVVSFSPSTTISVTPEGGPGGHSLQVLTLFLALTSALLLALIFITLLFSVLKWI 214

Qy        182 RQHMCPRETQPFAEVQLSA--EDACSFQFPEEERG 214
              |:       ||| :   :|  ||||| : |:|| |
Db        215 RKKFPHIFKQPFKKTTGAAQEEDACSCRCPQEEEG 249
```

RESULT 3
I48700
gene ox40 protein - mouse
N;Alternate names: OX40 antigen
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48700; I48334; S34377
R;Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.;
J. Immunol. 151, 5261-5271, 1993
A;Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell int
A;Reference number: I48700; MUID:94044750; PMID:8228223
A;Accession: I48700
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-272 <RES>
A;Cross-references: UNIPROT:P47741; EMBL:Z21674; NID:g312827; PIDN:CAA79772.1; PID:g3128
R;Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
Eur. J. Immunol. 25, 926-930, 1995
A;Title: Gene structure and chromosomal localization of the mouse homologue of rat OX40 r
A;Reference number: I48334; MUID:95255413; PMID:7737295
A;Accession: I48334
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-14,'G',16-272 <RE2>
A;Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819
C;Genetics:
A;Gene: ox40
A;Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C;Superfamily: CD27 antigen; NGF receptor repeat homology

  Query Match 10.3%; Score 134; DB 2; Length 272;
  Best Local Similarity 22.9%; Pred. No. 0.00057;
  Matches 66; Conservative 25; Mismatches 103; Indels 94; Gaps 15;

```
Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGK---EDCPK 57
              |  |       :|  | ||         |    |::   :  :||    ||      |
Db          1 MYVWVQQPTALLLLALTLG--VTARRLNC----VKHTYPSGHKCCRECQPGHGMVSRCDH 54

Qy         58 ER---C-ICVTPEYH-------CGDPQCKICKHYP----------------CQPGQRVE 89
              |   | | |  |:       |   ||  | |                  |:|| :
Db         55 TRDTLCHPCETGFYNEAVNYDTC--KQCTQCNHRSGSELKQNCTPTQDTVCRCRPGTQPR 112

Qy         90 SQGDIVFGFRCVACAMGTFSAGRDGHCRLWTNCSQFGFLTMFPGNKTHNAVC-------- 141
                | || |  | || | :  |: ||||:  |  |  | : : :|||
Db        113 QDSGYKLGVDCVPCPPGHFSPGNNQACKPWTNCTLSGKQTRHPASDSLDAVCEDRSLLAT 172

Qy        142 -------------------------IPEPLPT--EQYGHLTVIFLVMAACIFFLTTVQL 173
                                      :| | ||    |   : | :   :    || |
Db        173 LLWETQRPTFRPTTVQSTTVWPRTSELPSP-PTLVTPEGPAFAVLLGLGLGLLAPLTVLL 231

Qy        174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDAC---SFQFPEEERGEQTE 218
              |::  ||:    |   :|           |   ||: | :|  | |:
Db        232 ALYL--LRKAWRLPNTPKP----------CWGNSFRTPIQE--EHTD 264
```

RESULT 4
S12783
OX40 antigen precursor - rat
N;Alternate names: nerve growth factor receptor homolog
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: S12783; S08036
R;Mallett, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A;Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes
A;Reference number: S12783; MUID:90214614; PMID:2157591
A;Accession: S12783
A;Molecule type: mRNA
A;Residues: 1-271 <MAL>
A;Cross-references: UNIPROT:P15725; EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: growth factor receptor; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-271/Product: OX40 antigen #status predicted <MAT>
F;211-235/Domain: transmembrane #status predicted <TMM>

  Query Match 9.7%; Score 126.5; DB 2; Length 271;
  Best Local Similarity 21.6%; Pred. No. 0.0024;
  Matches 62; Conservative 27; Mismatches 105; Indels 93; Gaps 13;

```
Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGK---EDCPK 57
              |  |       :|  | ||    |  :  |     |::   :  :||    ||      |
Db          1 MYVWVQQPTAFLLLGLSLG---VTVKLNC----VKDTYPSGHKCCRECQPGHGMVSRCDH 53

Qy         58 ER---CICVTPEYH--------CGDPQCKICKH----------------YPCQPGQRVE 89
              |   |     | ::         |   ||  | |                  |:|| :
Db         54 TRDTVCHPCEPGFYNEAVNYDTC--KQCTQCNHRSGSELKQNCTPTEDTVCQCRPGTQPR 111

Qy         90 SQGDIVFGFRCVACAMGTFSAGRDGHCRLWTNCSQFGFLTMFPGNKTHNAVC-------- 141
```

```
Db        112 QDSSHKLGVDCVPCPPGHFSPGSNQACKPWTNCTLSGKQIRHPASNSLDTVCEDRSLLAT 171

Qy        142 --------------IPE-------------PLPTEQYGHLTVIFLVMAACIFFLTTVQLG 174
                           :|                |     |   : | :   :    || |
Db        172 LLWETQRTTFRPTTVPSTTVWPRTSQLPSTPTLVAPEGPAFAVILGLGLGLLAPLTVLLA 231

Qy        175 LHIWQLRRQHMCPRETQPFAEVQLSAEDAC---SFQFPEEERGEQTE 218
              |::  ||:    |   :|           |   ||: | :|  |||:
Db        232 LYL--LRKAWRSPNTPKP-----------CWGNSFRTPIQE--EQTD 263


RESULT 5
A49053
CD27 antigen precursor - mouse
N;Alternate names: CD27L receptor; T cell activation antigen CD27
C;Species: Mus musculus (house mouse)
C;Date: 19-Dec-1993 #sequence_revision 22-Apr-1995 #text_change 09-Jul-2004
C;Accession: A49053
R;Gravestein, L.A.; Blom, B.; Nolten, L.A.; de Vries, E.; van der Horst, G.; Ossendorp,
Eur. J. Immunol. 23, 943-950, 1993
A;Title: Cloning and expression of murine CD27: comparison with 4-1BB, another lymphocyt
A;Reference number: A49053; MUID:93209296; PMID:8384562
A;Accession: A49053
A;Molecule type: mRNA
A;Residues: 1-250 <GRA>
A;Cross-references: UNIPROT:P41272
A;Note: sequence extracted from NCBI backbone (NCBIN:128168, NCBIP:128169)
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; homodimer; receptor; surface antigen; T-cell; tra
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-250/Product: CD27 antigen #status predicted <MAT>
F;21-182/Domain: extracellular #status predicted <EXT>
F;27-63/Domain: NGF receptor repeat homology <NG1>
F;65-105/Domain: NGF receptor repeat homology <NG2>
F;121-179/Region: proline/serine/threonine-rich
F;183-202/Domain: transmembrane #status predicted <TMN>
F;203-250/Domain: intracellular #status predicted <INT>
F;95,162/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             9.6%;  Score 125.5;  DB 1;  Length 250;
  Best Local Similarity   20.8%;  Pred. No. 0.0027;
  Matches   55;  Conservative   30;  Mismatches   93;  Indels   87;  Gaps   13;

Qy          3 AWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGK---EDCPKER 59
              ||   | : ||  | :|  : :    |       | |    || :  ||    :|| ::|
Db          2 AWPPPYWLCMLGTL-VGLSATLAPNSCPDKHYWTGGG---LCCRMCEPGTFFVKDCEQDR 57

Qy         60 -------CI---CVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFS 109
                  ||      :|:||   | |: |:|  |  |  : :          |   |     |
Db         58 TAAQCDPCIPGTSFSPDYHT-RPHCESCRH--CNSGFLIRN---------CTVTANAECS 105

Qy        110 AGRDGHCR----------------------------------------LWTNCSQFGFLTM 130
                ::  ||                                        |    |    |:
Db        106 CSKNWQCRDQECTECDPPLNPALTRQPSETPSPQPPPTHLPHGTEKPSWPLHRQLPNSTV 165

Qy        131 FPGNKTHNAVCIPEPLPT-EQYGHLTVIFLVMAACIFFLTTVQLGLHIWQLRRQHMCPRE 189
              :    :|  :|  : :     :  : :|| |: | :||          || |
Db        166 YSQRSSHRPLCSSDCIRIFVTFSSMFLIF-VLGAILFF----------HQRRNH----- 208

Qy        190 TQPFAEVQLSAEDACSFQFPEEERG 214
                |  : |   |: | :  | || |
Db        209 -GPNEDRQAVPEEPCPYSCPREEEG 232


RESULT 6
I37552
OX40 homolog - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I37552
R;Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat
Eur. J. Immunol. 24, 677-683, 1994
A;Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment of
A;Reference number: I37552; MUID:94170844; PMID:7510240
A;Accession: I37552
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-277 <RES>
A;Cross-references: UNIPROT:P43489; EMBL:X75962; NID:g472957; PIDN:CAA53576.1; PID:g47295
C;Superfamily: CD27 antigen; NGF receptor repeat homology

  Query Match             9.4%;  Score 122;  DB 2;  Length 277;
  Best Local Similarity   21.1%;  Pred. No. 0.0057;
  Matches   54;  Conservative   22;  Mismatches   80;  Indels  100;  Gaps    8;

Qy         13 LCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERCICVTPEYHCGDP 72
              | :| ||  :|      |   | :   :| |||    ||     :           |
Db         16 LLLLGLGLSTVT-----GLHCVGDTYPSNDRCCHECRPGNGMVSR----------CSRS 59

Qy         73 QCKICKHYPCQPG-------------------------QRVESQGDIVF---------- 96
              |  :|:  || ||                        |.  :  | |
Db         60 QNTVCR--PCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLD 117

Qy         97 ----GFRCVACAMGTFSAGRDGHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYG 152
                  |  |  | || | :  |: ||||:  |  |: | : : :|:|     |  |
Db        118 SYKPGVDCAPCPPGHFSPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPATQ-- 175

Qy        153 HLTVIFLVMAACIFFLTTVQLGLHIWQLRRQHMCPRETQ--PFAEVQLSAEDACSFQFPE 210
                                                  |:|||  |   : :   :|    :|
Db        176 ---------------------------------PQETQGPPARPITVQPTEA----WPR 197

Qy        211 EERGEQTEEKCHLGGR 226
                :|  |     |||
Db        198 TSQGPSTRPVEVPGGR 213


RESULT 7
JE0315
low-density lipoprotein receptor-related protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: JE0315
R;Tomita, Y.; Kim, D.; Magoori, K.; Fujino, T.; Yamamoto, T.T.
J. Biochem. 124, 784-789, 1998
A;Title: A novel low-density lipoprotein receptor-related protein with type II membrane p
A;Reference number: JE0315; MUID:98429596; PMID:9756624
A;Accession: JE0315
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1113 <TOM>
A;Cross-references: UNIPROT:Q9Z319; DDBJ:AB013874; NID:g3869144; PIDN:BAA34371.1; PID:g38
C;Superfamily: mouse low-density lipoprotein receptor-related protein; LDL receptor ligan
F;337-372/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;374-408/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;410-445/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;447-482/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;648-682/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F;684-720/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F;723-757/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F;869-1097/Domain: trypsin homology <TRY>

  Query Match             9.1%;  Score 119;  DB 2;  Length 1113;
  Best Local Similarity   25.4%;  Pred. No. 0.035;
  Matches   75;  Conservative   26;  Mismatches   96;  Indels   98;  Gaps   20;

Qy         11 SMLC--VLDLGQPS--------VVEEPGCGPGK------VQNGSGNNTRC--------CS 46
              |:||    | | ||         : :|  || |:       | :|  :   |        ||
Db        390 SLLCDGYDDCGDPSDEQNCDCNLTKEHRCGDGRCIAAEWVCDGDHD---CVDKSDEVNCS 446

Qy         47 LYAPGKEDCPKERCICVTPEYHC-GDPQCK------IC--KHYPCQPGQRVESQGDIVFG 97
                :: |  :|   :||  |  : | ||  ||       |     ||  |:    ||   ||
Db        447 CHSQGLVECTSGQCIPST--FQCDGDEDCKDGSDEENCSDSQTPCPEGE----QG--CFG 498

Qy         98 FRCVACAMGTFSAGRDGHCRLWTNCSQFGFLTM--------------FPGNKTHNAVCI 142
                 ||    |:      |      :||||   :|:               : |::|     |
```

```
Db        499 SSCVESCAGSSLCDSDSSL---SNCSQCEPITLELCMNLLYNHTHYPNYLGHRTQKEASI 555

Qy        143 -------PEPLPTEQYGHLTVIFLVMAACIFFL--TTVQLGLHI--WQLRRQHMCPRETQ 191
                  |  : |  |       :|:  ||    :    |  |  |    :|  :|    |
Db        556 SWESSLFPALVQTNCYK-----YLMFFACTILVPKCDVNTGQRIPPCRLLCEHSKERCES 610

Qy        192 PFAEVQLS-AEDACSFQFPEEERGEQT--------EE-----------KCHLGGR 226
                | |    ||    |||||    ||         ||           :| || |
Db        611 VLGIVGLQWPEDTDCNQFPEESSDNQTCLLPNEDVEECSPSHFKCRSGRCVLGSR 665


RESULT 8
A60771
B-cell activation protein CD40 precursor - human
N;Alternate names: B-cell surface antigen Bp50
C;Species: Homo sapiens (man)
C;Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: S04460; A60771
R;Stamenkovic, I.; Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A;Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor
A;Reference number: S04460; MUID:89356608; PMID:2475341
A;Accession: S04460
A;Molecule type: mRNA
A;Residues: 1-277 <STA>
A;Cross-references: UNIPROT:P25942; EMBL:X60592; NID:g29850; PIDN:CAA43045.1; PID:g29851
R;Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A;Title: Biochemical characteristics and partial amino acid sequence of the receptor-lik
A;Reference number: A60771; MUID:89093941; PMID:2463309
A;Accession: A60771
A;Molecule type: protein
A;Residues: 21-50 <BRA>
A;Experimental source: Burkitt lymphoma cell line Raji
C;Genetics:
A;Gene: GDB:CD40
A;Cross-references: GDB:215268; OMIM:109535
A;Map position: 20q12-20q13.2
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
F;21-193/Domain: extracellular #status predicted <EXT>
F;194-215/Domain: transmembrane #status predicted <TMM>
F;216-277/Domain: intracellular #status predicted <CYT>
F;153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             9.1%;  Score 118.5;  DB 2;  Length 277;
  Best Local Similarity   21.0%;  Pred. No. 0.011;
  Matches   50;  Conservative   29;  Mismatches   88;  Indels   71;  Gaps   10;

Qy         41 NTRCCSLYAPGKE---DCPK---------------------------ERC---------- 60
              |::||||  ||::   || :                           : |
Db         34 NSQCCSLCQPGQKLVSDCTEFTETECLPCGESEFLDTWNRETHCHQHKYCDPNLGLRVQQ 93

Qy         61 --------ICVTPE-YHCGDPQCKIC-KHYPCQPGQRVESQGDIVFGFRCVACAMGTFS- 109
                     ||   | :||    |: |  |  | || |:     |     |  | :| ||
Db         94 KGTSETDTICTCEEGWHCTSEACESCVLHRSCSPGFGVKQIATGVSDTICEPCPVGFFSN 153

Qy        110 -AGRDGHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFL 168
               :     | ||:|     :    |    : || |:    ::   | || ::    :| :
Db        154 VSSAFEKCHPWTSCETKDLVVQQAGTNKTDVVCGPQ----DRLRALVVIPIIF-GILFAI 208

Qy        169 TTVQLGLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT----EEKCH 222
                | : :    :  :  |   |   |:          ||::  |  |    :|  |
Db        209 LLVLVFIKKVAKKPTNKAPHPKQEPQEI----------NFPDDLPGSNTAAPVQETLH 256


RESULT 9
I54182
tumor necrosis factor receptor 2-related protein - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C;Accession: I54182
R;Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A;Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequenc
A;Reference number: I54182; MUID:93252381; PMID:8486360
A;Accession: I54182
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-435 <RES>
A;Cross-references: UNIPROT:P36941; GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762
C;Genetics:
A;Gene: GDB:LTBR
A;Cross-references: GDB:1230195; OMIM:600979
A;Map position: 12p13.3-12p13.1
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog

  Query Match             8.8%;  Score 115;  DB 2;  Length 435;
  Best Local Similarity   22.2%;  Pred. No. 0.033;
  Matches   54;  Conservative   23;  Mismatches   94;  Indels   72;  Gaps   13;

Qy          3 AWAMLYGVSMLCVLDLGQPSVV-----EEPGCGPGKVQNGSGNNTRCCSLYAPG---KED 54
              ||  |  : :  :|   ||  |     |   |   : :     :  |||   ||
Db         13 AWGPLV-LGLFGLLLAASQPQAVPPYASENQTCRDQEKEYYEPQHRICCSRCPPGTYVSAK 71

Qy         55 CPKER-CICVTPEYHCG--------------------DP---------------QCKI- 76
              | : |  :| | |  |                    ||               ||:
Db         72 CSRIRDTVCAT----CAENSYNEHWNYLTICQLCRPCDPVMGLEEIAPCTSKRKTQCRCQ 127

Qy         77 -----------CKH----YPCQPGQRVESQGDIVFG-FRCVACAMGTF--SAGRDGHCRL 118
                         | |       | ||   | : ::  |   || |  | |  ::     |:
Db        128 PGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNNHCVPCKAGHFQNTSSPSARCQP 187

Qy        119 WTNCSQFGFLTMFPGNKTHNAVCIP--EPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLH 176
                | |   | :   ||    :  |    |||| |  | : ::  |:    |||    :
Db        188 HTRCENQGLVEAAPGTAQSDTTCKNPLEPLPPEMSGTM-LMLAVLLPLAFFLLLATVFSC 246

Qy        177 IWQ 179
              ||:
Db        247 IWK 249


RESULT 10
I48854
gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48854
R;Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A;Reference number: I48854; MUID:95178848; PMID:7873884
A;Accession: I48854
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-459 <RES>
A;Cross-references: UNIPROT:Q62327; EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g43383
C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolog
F;151-188/Domain: NGF receptor repeat homology <NGF>

  Query Match             8.3%;  Score 107.5;  DB 2;  Length 459;
  Best Local Similarity   26.1%;  Pred. No. 0.14;
  Matches   54;  Conservative   13;  Mismatches   63;  Indels   77;  Gaps   13;

Qy          4 WAMLYGVSMLCVLDLGQPSVVEEPG--------------------CGPGKVQNGSGNNT- 42
              ||  : |    ||   :|    |||                    | ||:     | |
Db          2 WATGHTVPAQVVLTPYKP----EPGYECQISQEYYDRKAQMCCAKCPPGQYVKHFCNKTS 57

Qy         43 --------------------RCCSLYAPGKED------CPKER---CICVTPEY-----H 68
                               | |  :    |       | |::   | |     |      |
Db         58 DTVCADCEASMYTQVWNQFRTCLSCSSSCSTDQVETRACTKQQNRVCACEAGRYCALKTH 117

Qy         69 CGDPQCKICKHY-PCQPGQRVES----QGDIVFGFRCVACAMGTFS--AGRDGHCRLWTN 121
                 |   |: |     | ||  | |     |:::    | ||| ||||        ||
```

```
Db        118 SG--SCRQCMRLSKCGPGFGVASSRAPNGNVL----CKACAPGTFSDTTSSTDVCRPHRI 171

Qy        122 CSQFGFLTMFPGNKTHNAVCIPEPLPT 148
              ||    :   ||| : :||| ||  ||
Db        172 CS----ILAIPGNASTDAVCAPES-PT 193


RESULT 11
B38634
tumor necrosis factor receptor type 2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: B38634; A40254; S54816
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor r
A;Reference number: A38634; MUID:91187885; PMID:1849278
A;Accession: B38634
A;Molecule type: mRNA
A;Residues: 1-474 <LEW>
A;Cross-references: UNIPROT:P25119; GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk
Mol. Cell. Biol. 11, 3020-3026, 1991
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for
A;Reference number: A40254; MUID:91246168; PMID:1645445
A;Accession: A40254
A;Molecule type: mRNA
A;Residues: 1-474 <GOO>
A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R;Kissonerghis, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y.
submitted to the EMBL Data Library, May 1995
A;Description: Characterization of the promoter region of the murine p75-TNF receptor.
A;Reference number: S54816
A;Accession: S54816
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-22 <KIS>
A;Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044
C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolo
C;Keywords: cytokine receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
F;40-77/Domain: NGF receptor repeat homology <NG1>
F;79-120/Domain: NGF receptor repeat homology <NG2>
F;166-203/Domain: NGF receptor repeat homology <NG4>

  Query Match             8.2%;  Score 106.5;  DB 2;  Length 474;
  Best Local Similarity   26.1%;  Pred. No. 0.18;
  Matches   54;  Conservative   13;  Mismatches   63;  Indels   77;  Gaps   13;

Qy          4 WAMLYGVSMLCVLDLGQPSVVEEPG--------------------CGPGKVQNGSGNNT- 42
              ||  : |    ||   :|    |||                    | ||:      | |
Db         17 WATGHTVPAQVVLTPYKP----EPGYECQISQEYYDRKAQMCCAKCPPGQYVKHFCNKTS 72

Qy         43 --------------------RCCSLYAPGKED------CPKER---CICVTPEY-----H 68
                               | |  :    |       | |::   | |     |     |
Db         73 DTVCADCEASMYTQVWNQFRTCLSCSSSCTTDQVEIRACTKQQNRVCACEAGRYCALKTH 132

Qy         69 CGDPQCKICKHY-PCQPGQRVES----QGDIVFGFRCVACAMGTFS--AGRDGHCRLWTN 121
               |   |: |      | ||  | |      |:::    | ||| ||||         ||
Db        133 SG--SCRQCMRLSKCGPGFGVASSRAPNGNVL----CKACAPGTFSDTTSSTDVCRPHRI 186

Qy        122 CSQFGFLTMFPGNKTHNAVCIPEPLPT 148
              ||    :   ||| : :||| ||  ||
Db        187 CS----ILAIPGNASTDAVCAPES-PT 208


RESULT 12
A46476
B cell-associated surface molecule CD40, long splice form - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46476; A46515
R;Torres, R.M.; Clark, E.A.
J. Immunol. 148, 620-626, 1992
A;Title: Differential increase of an alternatively polyadenylated mRNA species of murine
A;Reference number: A46476; MUID:92105763; PMID:1370315
A;Accession: A46476
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-305 <TOR>
A;Cross-references: UNIPROT:P27512; GB:M83312; NID:g1553058
A;Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)
A;Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0
R;Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne,
J. Immunol. 149, 3921-3926, 1992
A;Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A;Reference number: A46515; MUID:93094586; PMID:1281194
A;Accession: A46515
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-287,'LV' <GRI>
A;Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126; NI
A;Experimental source: BALB/c, liver
A;Note: sequence extracted from NCBI backbone (NCBIP:120357)
C;Comment: For an alternative splice form, see PIR:A46515.
C;Comment: For an alternative splice form, see PIR:A46476.
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: alternative splicing; transmembrane protein
F;105-144/Domain: NGF receptor repeat homology <NGF>

  Query Match             8.0%;  Score 104.5;  DB 2;  Length 305;
  Best Local Similarity   25.2%;  Pred. No. 0.18;
  Matches   38;  Conservative   13;  Mismatches   71;  Indels   29;  Gaps    8;

Qy         17 DLGQP--------SVVEEPGCGP---GKVQNGSGNNTRC-----CSLYAPG------KED 54
              || ||          : :|:  | |   |:          ||      |       |        ||
Db         39 DLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQHRHCE---PNQGLRVKKEG 95

Qy         55 CPKERCICVTPE-YHCGDPQCKIC-KHYPCQPGQRVESQGDIVFGFRCVACAMGTFS--A 110
                 :   :|   |  ||    |: | :| || ||  |           |  | :| ||  :
Db         96 TAESDTVCTCKEGQHCTSKDCEACAQHTPCIPGFGVMEMATETTDTVCHPCPVGFFSNQS 155

Qy        111 GRDGHCRLWTNCSQFGFLTMFPGNKTHNAVC 141
                |  ||:|       :  |    | :|
Db        156 SLFEKCYPWTSCEDKNLEVLQKGTSQTNVIC 186


RESULT 13
A35356
tumor necrosis factor receptor 2 precursor [validated] - human
N;Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094
R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K.
Science 248, 1019-1023, 1990
A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular and
A;Reference number: A35356; MUID:90260639; PMID:2160731
A;Accession: A35356
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-461 <SMI>
A;Cross-references: UNIPROT:P20333; GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186
R;Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires,
Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A;Title: A second tumor necrosis factor receptor gene product can shed a naturally occur
A;Reference number: A36475; MUID:91045991; PMID:2172983
A;Accession: A36475
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-195,'R',197-461 <KOH>
A;Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
R;Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.;
Cytokine 2, 231-237, 1990
A;Title: Two human TNF receptors have similar extracellular, but distinct intracellular,
```

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A;Reference number: A48416; MUID:91370690; PMID:1966549
A;Accession: A48416
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 23-461 <DEM>
A;Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649
A;Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBIP:63371)
R;Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A;Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra
A;Reference number: A36007; MUID:90349572; PMID:2166946
A;Accession: A36007
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 116-140,'P',142-195,'R',197-362,'T',364-461 <HEL>
A;Cross-references: GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:g339752
R;Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
J. Biol. Chem. 265, 20131-20138, 1990
A;Title: Purification and partial amino acid sequence analysis of two distinct tumor nec
A;Reference number: A23666; MUID:91056048; PMID:2173696
A;Accession: A23666
A;Status: preliminary
A;Molecule type: protein
A;Residues: 23-40;65-69;136-141;300-306 <LOE>
R;Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A;Reference number: A35010; MUID:90110215; PMID:2153136
A;Accession: B35010
A;Status: preliminary
A;Molecule type: protein
A;Residues: 27-31 <ENG>
R;Kuhnert, P.; Kemper, O.; Wallach, D.
Gene 150, 381-386, 1994
A;Title: Cloning, sequencing and partial functional characterization of the 5' region of
A;Reference number: I38094; MUID:95121934; PMID:7821811
A;Accession: I38094
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-37 <RES>
A;Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701
C;Genetics:
A;Gene: GDB:TNFR2
A;Cross-references: GDB:125914; OMIM:191191
A;Map position: 1p36.2-1p36.2
A;Introns: 26/3
A;Note: the list of introns is incomplete
C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolo
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
F;40-76/Domain: NGF receptor repeat homology <NG1>
F;78-119/Domain: NGF receptor repeat homology <NG2>
F;120-162/Domain: NGF receptor repeat homology <NG3>
F;164-201/Domain: NGF receptor repeat homology <NG4>
F;262-279/Domain: transmembrane #status predicted <TMN>
F;280-461/Domain: intracellular #status predicted <INT>
F;171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             7.9%;  Score 102.5;  DB 1;  Length 461;
  Best Local Similarity   22.4%;  Pred. No. 0.38;
  Matches   52;  Conservative   18;  Mismatches   67;  Indels   95;  Gaps   12;

Qy         29 CGPG---KVQNGSGNNTRC-----------------------CSLYAPGKEDCPKER-- 59
              | ||   ||     ::| |                       ||      : | :|:
Db         57 CSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNR 116

Qy         60 -CICVTPEYHCG---DPQCKICKHY-PCQPGQRVESQGDIVFGFRCVACAMGTFS--AGR 112
               | |  | ::|       |::|     |:|| |   |        |  || ||||
Db        117 ICTC-RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSS 175

Qy        113 DGHCRLWTNCSQFGFLTMFPGNKTHNAVC--------------IPEPLPTEQYGHLTVI 157
                    ||    |:    :   ||| : :|||              :|:|: |
```

```
Db        176 TDICRPHQICN----VVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVST--------- 222

Qy        158 FLVMAACIFFLTTVQLGLHIWQLRRQHMCPRETQPPAEVQLSAEDACSFQFP 209
                                    | ||     |||  |   |   : ||  |
Db        223 ----------------------RSQH-----TQPTPEP--STAPSTSFLLP 244


RESULT 14
TVRTNU
protein-tyrosine kinase (EC 2.7.1.112) neu precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A24562; A61204
R;Bargmann, C.I.; Hung, M.C.; Weinberg, R.A.
Nature 319, 226-230, 1986
A;Title: The neu oncogene encodes an epidermal growth factor receptor-related protein.
A;Reference number: A24562; MUID:86118662; PMID:3945311
A;Accession: A24562
A;Molecule type: mRNA
A;Residues: 1-1260 <BAR>
A;Cross-references: UNIPROT:P06494; EMBL:X03362; NID:g56745; PIDN:CAA27059.1; PID:g56746
R;Masui, T.; Mann, A.M.; Macatee, T.L.; Garland, E.M.; Okamura, T.; Smith, R.A.; Cohen, S
Carcinogenesis 12, 1975-1978, 1991
A;Title: Direct DNA sequencing of the rat neu oncogene transmembrane domain reveals no mu
2-thiazolyl]formamide or N-methyl-N-nitrosourea.
A;Reference number: A61204; MUID:92035293; PMID:1682063
A;Accession: A61204
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 637-663,'V',665-702 <MAS>
A;Note: authors translated the codon GCA for residue 25 as Val
C;Genetics:
A;Gene: neu
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosphot
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1260/Product: protein-tyrosine kinase neu #status predicted <MAT>
F;658-680/Domain: transmembrane #status predicted <TMN>
F;723-988/Domain: protein kinase homology <KIN>
F;731-739/Region: protein kinase ATP-binding motif
F;71,191,263,535,576,634/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;691/Binding site: phosphate (Thr) (covalent) #status predicted
F;758/Active site: Lys #status predicted
F;882,1227,1253/Binding site: phosphate (Tyr) (covalent) #status predicted

  Query Match             7.9%;  Score 102.5;  DB 1;  Length 1260;
  Best Local Similarity   26.6%;  Pred. No. 0.92;
  Matches   46;  Conservative   21;  Mismatches   73;  Indels   33;  Gaps    9;

Qy         30 GPGKVQNGSGNNTRC--CSLYAPGKEDCPKERCICVTPEYHCGDPQCKICKHYPCQPGQR 87
              |||          |:|  || :  |:|   : |      |  :  | :|  | |  |||
Db        527 GPGP--------TQCVNCSHFLRGQECVEECRVWKGLPREYVSDKRCLPC-HPECQP--- 574

Qy         88 VESQGDIVFGF---RCVACAMGTFSAGRDGHC-----------RLWTNCSQFGFLTMFPG 133
               ::  :  ||    :| |||    |:      |             :|    : |      |
Db        575 -QNSSETCFGSEADQCAACAHYKDSSSCVARCPSGVKPDLSYMPIWKYPDEEGICQPCPI 633

Qy        134 NKTHNAVCIPE-PLPTEQYGH--LTVIFLVMAACIFFLTTVQLGLHIWQLRRQ 183
              | ||: | : |   | ||       :|  |    :| :  | :|: | | : |||
Db        634 NCTHSCVDLDERGCPAEQRASPVTFIIATVEGVLLFLILVVVVGILI-KRRRQ 685


RESULT 15
A53102
alpha-2-macroglobulin receptor precursor - chicken
N;Alternate names: CD91; LDL receptor-related protein 1; low density lipoprotein receptor
C;Species: Gallus gallus (chicken)
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
C;Accession: A53102
R;Nimpf, J.; Stifani, S.; Bilous, P.T.; Schneider, W.J.
J. Biol. Chem. 269, 212-219, 1994
A;Title: The somatic cell-specific low density lipoprotein receptor-related protein of th
A;Reference number: A53102; MUID:94103212; PMID:7506255
```

A;Accession: A53102
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-4543 <NIM>
A;Cross-references: UNIPROT:P98157; GB:X74904; NID:g438006; PIDN:CAA52870.1; PID:g438007
C;Complex: The alpha-2-macroglobulin receptor complex consists of noncovalently-associat
d protein.
C;Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding
C;Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; calcium binding; glycopro
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-3942/Domain: alpha-2-macroglobulin receptor 515K chain #status predicted <515K>
F;18-3942,3943-4543/Product: alpha-2-macroglobulin receptor #status predicted <MAT>
F;29-66/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;74-110/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;117-150/Domain: EGF homology <EG1>
F;156-190/Domain: EGF homology <EG2>
F;200-241/Domain: LDL receptor YWTD-containing repeat homology <YW01>
F;242-283/Domain: LDL receptor YWTD-containing repeat homology <YW02>
F;294-336/Domain: LDL receptor YWTD-containing repeat homology <YW03>
F;337-380/Domain: LDL receptor YWTD-containing repeat homology <YW04>
F;381-422/Domain: LDL receptor YWTD-containing repeat homology <YW05>
F;423-470/Domain: LDL receptor YWTD-containing repeat homology <YW06>
F;480-521/Domain: EGF homology <EG3>
F;573-615/Domain: LDL receptor YWTD-containing repeat homology <YW07>
F;616-661/Domain: LDL receptor YWTD-containing repeat homology <YW08>
F;662-712/Domain: LDL receptor YWTD-containing repeat homology <YW09>
F;713-754/Domain: LDL receptor YWTD-containing repeat homology <YW10>
F;755-797/Domain: LDL receptor YWTD-containing repeat homology <YW11>
F;805-840/Domain: EGF homology <EG4>
F;852-888/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;893-929/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;934-969/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F;974-1009/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F;1013-1049/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F;1060-1095/Domain: LDL receptor ligand-binding repeat homology <LDL8>
F;1102-1138/Domain: LDL receptor ligand-binding repeat homology <LDL9>
F;1143-1180/Domain: LDL receptor ligand-binding repeat homology <LDLA>
F;1183-1219/Domain: EGF homology <EG5>
F;1225-1259/Domain: EGF homology <EG6>
F;1267-1306/Domain: LDL receptor YWTD-containing repeat homology <YW12>
F;1307-1353/Domain: LDL receptor YWTD-containing repeat homology <YW13>
F;1354-1396/Domain: LDL receptor YWTD-containing repeat homology <YW14>
F;1397-1443/Domain: LDL receptor YWTD-containing repeat homology <YW15>
F;1444-1486/Domain: LDL receptor YWTD-containing repeat homology <YW16>
F;1487-1529/Domain: LDL receptor YWTD-containing repeat homology <YW17>
F;1538-1576/Domain: EGF homology <EG7>
F;1581-1624/Domain: LDL receptor YWTD-containing repeat homology <YW18>
F;1625-1667/Domain: LDL receptor YWTD-containing repeat homology <YW19>
F;1668-1711/Domain: LDL receptor YWTD-containing repeat homology <YW20>
F;1712-1751/Domain: LDL receptor YWTD-containing repeat homology <YW21>
F;1752-1794/Domain: LDL receptor YWTD-containing repeat homology <YW22>
F;1795-1842/Domain: LDL receptor YWTD-containing repeat homology <YW23>
F;1846-1882/Domain: EGF homology <EG8>
F;1930-1972/Domain: LDL receptor YWTD-containing repeat homology <YW24>
F;1973-2015/Domain: LDL receptor YWTD-containing repeat homology <YW25>
F;2016-2059/Domain: LDL receptor YWTD-containing repeat homology <YW26>
F;2060-2101/Domain: LDL receptor YWTD-containing repeat homology <YW27>
F;2102-2147/Domain: LDL receptor YWTD-containing repeat homology <YW28>
F;2155-2190/Domain: EGF homology <EG9>
F;2195-2237/Domain: LDL receptor YWTD-containing repeat homology <YW29>
F;2247-2288/Domain: LDL receptor YWTD-containing repeat homology <YW30>
F;2338-2382/Domain: LDL receptor YWTD-containing repeat homology <YW31>
F;2383-2423/Domain: LDL receptor YWTD-containing repeat homology <YW32>
F;2424-2467/Domain: LDL receptor YWTD-containing repeat homology <YW33>
F;2476-2511/Domain: EGF homology <EG10>
F;2518-2555/Domain: LDL receptor ligand-binding repeat homology <LDLB>
F;2560-2594/Domain: LDL receptor ligand-binding repeat homology <LDLC>
F;2599-2633/Domain: LDL receptor ligand-binding repeat homology <LDLD>
F;2646-2682/Domain: LDL receptor ligand-binding repeat homology <LDLE>
F;2690-2724/Domain: LDL receptor ligand-binding repeat homology <LDLF>
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F;2772-2810/Domain: LDL receptor ligand-binding repeat homology <LDLH>
F;2816-2851/Domain: LDL receptor ligand-binding repeat homology <LDLI>
F;2856-2895/Domain: LDL receptor ligand-binding repeat homology <LDLJ>
F;2902-2936/Domain: LDL receptor ligand-binding repeat homology <LDLK>
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F;2983-3018/Domain: EGF homology <EG12>
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F;3154-3197/Domain: LDL receptor YWTD-containing repeat homology <YW37>
F;3198-3238/Domain: LDL receptor YWTD-containing repeat homology <YW38>
F;3239-3281/Domain: LDL receptor YWTD-containing repeat homology <YW39>
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F;3450-3486/Domain: LDL receptor ligand-binding repeat homology <LDLO>
F;3491-3528/Domain: LDL receptor ligand-binding repeat homology <LDLP>
F;3533-3567/Domain: LDL receptor ligand-binding repeat homology <LDLQ>
F;3572-3606/Domain: LDL receptor ligand-binding repeat homology <LDLR>
F;3610-3644/Domain: LDL receptor ligand-binding repeat homology <LDLS>
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F;3692-3728/Domain: LDL receptor ligand-binding repeat homology <LDLU>
F;3738-3774/Domain: LDL receptor ligand-binding repeat homology <LDLV>
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F;3826-3858/Domain: EGF homology <EG15>
F;3866-3909/Domain: LDL receptor YWTD-containing repeat homology <YW40>
F;3910-3968/Domain: LDL receptor YWTD-containing repeat homology <YW41>
F;3943-4543/Domain: alpha-2-macroglobulin receptor 85K chain #status predicted <85K>
F;3943-4420/Domain: 85K chain extracellular #status predicted <EXT>
F;3969-4011/Domain: LDL receptor YWTD-containing repeat homology <YW42>
F;4012-4055/Domain: LDL receptor YWTD-containing repeat homology <YW43>
F;4056-4098/Domain: LDL receptor YWTD-containing repeat homology <YW44>
F;4099-4141/Domain: LDL receptor YWTD-containing repeat homology <YW45>
F;4150-4181/Domain: EGF homology <EG16>
F;4199-4230/Domain: EGF homology <EG17>
F;4235-4266/Domain: EGF homology <EG18>
F;4271-4302/Domain: EGF homology <EG19>
F;4307-4338/Domain: EGF homology <EG20>
F;4343-4373/Domain: EGF homology <EG21>
F;4376-4408/Domain: EGF homology <EG22>
F;4421-4443/Domain: transmembrane #status predicted <TMM>
F;4444-4543/Domain: intracellular #status predicted <INT>
F;116,138,187,276,359,448,731,926,1048,1152,1153,1193,1216,1305,1509,1556,1573,1614,1643,
3485,3659,3786,3837,3952,4074,4124,4178,4278/Binding site: carbohydrate (Asn) (covalent)
F;168,2995/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F;2955/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted

Query Match 7.9%; Score 102.5; DB 1; Length 4543;
Best Local Similarity 28.0%; Pred. No. 2.9;
Matches 47; Conservative 12; Mismatches 44; Indels 65; Gaps 14;

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Qy          5 AMLYGVSMLC--VLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERCIC 62
              :: |  | :|    | |  |  :|  | ||      |   :| : |     ||  |||
Db       2658 SLCYAPSWVCDGANDCGDYS--DERNC-PG------GRKPKCPANYFA----CPSGRCIP 2704

Qy         63 VT------------PEYHCGDPQCKICKHYPCQPGQRVESQGDIVF---GFRCVA---- 102
              :|              | || : | | |  || |             |    ||::
Db       2705 MTWTCDKEDDCENGEDETHCSERQDKFC--YPVQ-----------PECNNHRCISKLWV 2750

Qy        103 ------CAMGTFSAGRDGHCRLWTNCSQFGFLTMFPGNKTHNAVCIPE 144
                   |  |   :  |  ||| | ||   |    ||      ||:||
Db       2751 CDGADDCGDG---SDEDSRCRL-TTCSTGSF--QCPG----TYVCVPE 2788
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Search completed: October 26, 2005, 15:52:33
Job time : 27.307 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 26, 2005, 15:29:08 ; Search time 112.299 Seconds
(without alignments)
1039.676 Million cell updates/sec

Title: US-09-545-998B-2
Perfect score: 1301
Sequence: 1 MGAWAMLYGVSMLCVLDLGQ.....PEEERGEQTEEKCHLGGRWP 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1301	100.0	228	1	TR18_MOUSE	O35714 mus musculu
2	1294	99.5	250	2	Q8C4K3	Q8c4k3 mus musculu
3	735.5	56.5	241	1	TR18_HUMAN	Q9y5u5 homo sapien
4	228.5	17.6	255	1	TNR9_HUMAN	Q07011 homo sapien
5	203.5	15.6	256	1	TNR9_MOUSE	P20334 mus musculu
6	184	14.1	211	2	Q8R037	Q8r037 mus musculu
7	175	13.5	276	2	Q9DDD2	Q9ddd2 gallus gall
8	154	11.8	275	2	Q80WM9	Q80wm9 mus musculu
9	149.5	11.5	276	2	Q71F55	Q71f55 mus musculu
10	145.5	11.2	196	2	Q8VC17	Q8vc17 mus musculu
11	139	10.7	318	2	Q7T2H3	Q7t2h3 oncorhynchu
12	138.5	10.6	270	2	Q75SV8	Q75sv8 felis silve
13	137.5	10.6	290	2	Q76LB4	Q76lb4 paralichthy
14	136	10.5	401	2	Q6PI12	Q6pi12 mus musculu
15	135.5	10.4	467	2	Q800I0	Q800i0 gallus gall
16	134	10.3	272	1	TNR4_MOUSE	P47741 mus musculu
17	128	9.8	401	1	T11B_MOUSE	O08712 mus musculu
18	127.5	9.8	267	2	O02764	O02764 oryctolagus
19	127	9.8	278	2	Q8SQ34	Q8sq34 sus scrofa
20	127	9.8	401	1	T11B_RAT	O08727 rattus norv
21	126.5	9.7	271	1	TNR4_RAT	P15725 rattus norv
22	125.5	9.6	250	1	TNR7_MOUSE	P41272 mus musculu
23	125	9.6	625	1	TR11_MOUSE	O35305 mus musculu
24	122	9.4	277	1	TNR4_HUMAN	P43489 homo sapien
25	122	9.4	401	1	T11B_HUMAN	O00300 homo sapien
26	121.5	9.3	269	1	TNR5_BOVIN	Q28203 bos taurus
27	120.5	9.3	415	1	TNR3_MOUSE	P50284 mus musculu
28	120	9.2	616	1	TR11_HUMAN	Q9y6q6 homo sapien
29	119.5	9.2	274	2	Q7YRL5	Q7yrl5 canis famil
30	119.5	9.2	277	2	Q8WMQ2	Q8wmq2 ovis aries
31	119	9.1	1113	1	CORI_MOUSE	Q9z319 mus musculu
32	118.5	9.1	277	1	TNR5_HUMAN	P25942 homo sapien
33	118.5	9.1	387	2	Q6GLN3	Q6gln3 xenopus lae
34	115.5	8.9	223	2	Q86YK5	Q86yk5 homo sapien
35	115.5	8.9	302	2	Q9PUS0	Q9pus0 salvelinus
36	115	8.8	435	1	TNR3_HUMAN	P36941 homo sapien
37	114	8.8	308	1	ZDH7_HUMAN	Q9nxf8 homo sapien
38	110.5	8.5	300	1	TR6B_HUMAN	O95407 homo sapien
39	110.5	8.5	461	2	Q6VAU8	Q6vau8 rattus norv
40	110.5	8.5	474	1	TR1B_RAT	Q80wy6 rattus norv
41	110.5	8.5	1259	2	Q8K3F9	Q8k3f9 rattus norv
42	108.5	8.3	186	2	Q7ZZY5	Q7zzy5 gallus gall
43	108	8.3	285	2	Q90W71	Q90w71 oncorhynchu
44	107.5	8.3	169	2	Q9JKE0	Q9jke0 rattus norv
45	107.5	8.3	459	2	Q62327	Q62327 mus musculu

ALIGNMENTS

RESULT 1
TR18_MOUSE
ID TR18_MOUSE STANDARD; PRT; 228 AA.
AC O35714; Q9JKR1; Q9JKR2; Q9JKR3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 18 precursor
DE (Glucocorticoid-induced TNFR-related protein).
GN Name=Tnfrsf18; Synonyms=Gitr;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC STRAIN=C3H;
RX MEDLINE=97322352; PubMed=9177197; DOI=10.1073/pnas.94.12.6216;
RA Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A.,
RA Moraca R., Migliorati G., Riccardi C.;
RT "A new member of the tumor necrosis factor/nerve growth factor
RT receptor family inhibits T cell receptor-induced apoptosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC STRAIN=BALB/c;
RX MEDLINE=20256302; PubMed=10798444; DOI=10.1089/104454900314474;
RA Nocentini G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A.,
RA Delfino D., Migliorati G., Riccardi C.;
RT "Gene structure and chromosomal assignment of mouse GITR, a member of
RT the tumor necrosis factor/nerve growth factor receptor family.";
RL DNA Cell Biol. 19:205-217(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS B; C AND D).
RC TISSUE=Thymus;
RX MEDLINE=20292073; PubMed=10836847;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Brunetti L., Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GITR.";
RL Cell Death Differ. 7:408-410(2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

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RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
CC   -!- FUNCTION: Receptor for TNFSF18. Seems to be involved in
CC       interactions between activated T lymphocytes and endothelial cells
CC       and in the regulation of T cell receptor-mediated cell death.
CC       Mediated NF-kappa-B activation via the TRAF2/NIK pathway (By
CC       similarity).
CC   -!- SUBUNIT: Binds to TRAF1, TRAF2, and TRAF3, but not TRAF5 and TRAF6
CC       (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms A, B and
CC       C); secreted (isoform D).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Name=A;
CC         IsoId=O35714-1; Sequence=Displayed;
CC       Name=B;
CC         IsoId=O35714-2; Sequence=VSP_006510;
CC       Name=C;
CC         IsoId=O35714-3; Sequence=VSP_006511;
CC       Name=D;
CC         IsoId=O35714-4; Sequence=VSP_006509;
CC   -!- TISSUE SPECIFICITY: Preferentially expressed in activated T
CC       lymphocytes.
CC   -!- INDUCTION: Up-regulated in peripherical mononuclear cells after
CC       antigen stimulation/lymphocyte activation.
CC   -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U82534; AAB81243.1; -.
DR   EMBL; AF109216; AAF14231.1; -.
DR   EMBL; AF229432; AAF61566.1; -.
DR   EMBL; AF229433; AAF61567.1; -.
DR   EMBL; AF229434; AAF61568.1; -.
DR   EMBL; AK020762; BAC25639.1; -.
DR   MGD; MGI:894675; Tnfrsf18.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR001368; TNFR_c6.
DR   SMART; SM00181; EGF; 1.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
DR   PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
KW   Alternative splicing; Glycoprotein; Receptor; Repeat; Signal;
KW   Transmembrane.
FT   SIGNAL        1     19       Potential.
FT   CHAIN        20    228       Tumor necrosis factor receptor
FT                                superfamily member 18.
FT   DOMAIN       20    153       Extracellular (Potential).
FT   TRANSMEM    154    174       Potential.
FT   DOMAIN      175    228       Cytoplasmic (Potential).
FT   REPEAT       28     61       TNFR-Cys 1.
FT   REPEAT       62    101       TNFR-Cys 2.
FT   REPEAT      102    142       TNFR-Cys 3.
FT   DISULFID     29     44       By similarity.
FT   DISULFID     62     74       By similarity.
FT   DISULFID     69     82       By similarity.
FT   DISULFID    103    122       By similarity.
FT   DISULFID    116    141       By similarity.
FT   CARBOHYD     36     36       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     40     40       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    121    121       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    134    134       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC    121    228       NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVM
FT                                AACIFFLTTVQLGLHIWQLRRQHMCPRETQPFAEVQLSAED
FT                                ACSFQFPEEERGEQTEEKCHLGGRWP -> KDPAIRGGAVV
FT                                S (in isoform D).
FT                                /FTId=VSP_006509.
FT   VARSPLIC    189    228       ETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP
FT                                -> VLLQRPSHSRRCSCQLRMLAASSSLRRNAGSRQKKSVI
FT                                WGVGGHEAWSSSVPQARRYKTCPAIPLVRAGAMLCTLPWAW
FT                                PCSPQQWRKWVYESGELRLGPMAAFLI (in isoform
FT                                B).
FT                                /FTId=VSP_006510.
FT   VARSPLIC    189    228       ETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP
FT                                -> GQLCPREGENVSQAPHLPQFYYRDPAIRGGAVVS (in
FT                                isoform C).
FT                                /FTId=VSP_006511.
SQ   SEQUENCE   228 AA;  25334 MW;  50D8C275D9C56259 CRC64;
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  Query Match             100.0%;  Score 1301;  DB 1;  Length 228;
  Best Local Similarity   100.0%;  Pred. No. 5.3e-106;
  Matches  228;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60

Qy         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120

Qy        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180
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Db        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180

Qy        181 RRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP 228
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Db        181 RRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP 228
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RESULT 2
Q8C4K3
ID   Q8C4K3      PRELIMINARY;      PRT;   250 AA.
AC   Q8C4K3;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched
DE   library, clone:C130084C11 product:tumor necrosis factor receptor
DE   superfamily, member 18, full insert sequence.
GN   Name=Tnfrsf18;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
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RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK081878; BAC38357.1; -.
DR   MGD; MGI:894675; Tnfrsf18.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR001368; TNFR_c6.
DR   SMART; SM00181; EGF; 1.
DR   SMART; SM00208; TNFR; 2.
KW   Receptor.
SQ   SEQUENCE   250 AA;  27814 MW;  6963E94F414C16B4 CRC64;

  Query Match             99.5%;  Score 1294;  DB 2;  Length 250;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-105;
  Matches  227;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60

Qy         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120

Qy        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180

Qy        181 RRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRW 227
              |||||||||||||||||||||||||||||||||||||||||||||||

Db        181 RRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRW 227


RESULT 3
TR18_HUMAN
ID   TR18_HUMAN     STANDARD;      PRT;   241 AA.
AC   Q9Y5U5; O95851; Q9NYJ9;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   25-JAN-2005 (Rel. 46, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 18 precursor
DE   (Glucocorticoid-induced TNFR-related protein) (Activation-inducible
DE   TNFR family receptor) (UNQ319/PRO364).
GN   Name=TNFRSF18; Synonyms=AITR, GITR;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1), AND INTERACTIONS WITH TRAF1; TRAF2 AND
RP   TRAF3.
RC   TISSUE=Bone marrow;
RX   MEDLINE=99175482; PubMed=10074428; DOI=10.1016/S0960-9822(99)80093-1;
RA   Gurney A.L., Marsters S.A., Huang R.M., Pitti R.M., Mark D.T.,
RA   Baldwin D.T., Gray A.M., Dowd A.D., Brush A.D., Heldens A.D.,
RA   Schow A.D., Goddard A.D., Wood W.I., Baker K.P., Godowski P.J.,
RA   Ashkenazi A.;
RT   "Identification of a new member of the tumor necrosis factor family
RT   and its receptor, a human ortholog of mouse GITR.";
RL   Curr. Biol. 9:215-218(1999).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=T-cell;
RX   MEDLINE=99156876; PubMed=10037686; DOI=10.1074/jbc.274.10.6056;
RA   Kwon B., Yu K.-Y., Ni J., Yu G.-L., Jang I.-K., Kim Y.-J., Xing L.,
RA   Liu D., Wang S.-X., Kwon B.S.;
RT   "Identification of a novel activation-inducible protein of the tumor
RT   necrosis factor receptor superfamily and its ligand.";
RL   J. Biol. Chem. 274:6056-6061(1999).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Thymus;
RX   MEDLINE=20292073; PubMed=10836847;
RA   Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA   Brunetti L., Migliorati G., Riccardi C.;
RT   "Identification of three novel mRNA splice variants of GITR.";
RL   Cell Death Differ. 7:408-410(2000).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
RA   Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA   Godowski P., Gray A.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
RN   [5]
RP   SEQUENCE OF 26-40.
```

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RX   PubMed=15340161; DOI=10.1110/ps.04682504;
RA   Zhang Z., Henzel W.J.;
RT   "Signal peptide prediction based on analysis of experimentally
RT   verified cleavage sites.";
RL   Protein Sci. 13:2819-2824(2004).
CC   -!- FUNCTION: Receptor for TNFSF18. Seems to be involved in
CC       interactions between activated T lymphocytes and endothelial cells
CC       and in the regulation of T cell receptor-mediated cell death.
CC       Mediated NF-kappa-B activation via the TRAF2/NIK pathway.
CC   -!- SUBUNIT: Binds to TRAF1, TRAF2, and TRAF3, but not TRAF5 and
CC       TRAF6.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).
CC       Secreted (isoform 2).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=Q9Y5U5-1; Sequence=Displayed;
CC       Name=2; Synonyms=GITR-D;
CC         IsoId=Q9Y5U5-2; Sequence=VSP_006508;
CC   -!- TISSUE SPECIFICITY: Expressed in lymph node, peripheral blood
CC       leukocytes and weakly in spleen.
CC   -!- INDUCTION: Up-regulated in peripherical mononuclear cells after
CC       antigen stimulation/lymphocyte activation.
CC   -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF125304; AAD22635.1; -.
DR   EMBL; AF117297; AAD19694.1; -.
DR   EMBL; AF241229; AAF63506.1; -.
DR   EMBL; AY358877; AAQ89236.1; -.
DR   Genew; HGNC:11914; TNFRSF18.
DR   MIM; 603905; -.
DR   GO; GO:0005031; F:tumor necrosis factor receptor activity; TAS.
DR   GO; GO:0006916; P:anti-apoptosis; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR001368; TNFR_c6.
DR   PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
DR   PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
KW   Alternative splicing; Direct protein sequencing; Glycoprotein;
KW   Receptor; Repeat; Signal; Transmembrane.
FT   SIGNAL       1     25
FT   CHAIN        26    241       Tumor necrosis factor receptor
FT                                superfamily member 18.
FT   DOMAIN       26    162       Extracellular (Potential).
FT   TRANSMEM     163   183       Potential.
FT   DOMAIN       184   241       Cytoplasmic (Potential).
FT   REPEAT       34    72        TNFR-Cys 1.
FT   REPEAT       74    112       TNFR-Cys 2.
FT   REPEAT       115   153       TNFR-Cys 3.
FT   DISULFID     34    49        By similarity.
FT   DISULFID     74    86        By similarity.
FT   DISULFID     81    94        By similarity.
FT   DISULFID     115   134       By similarity.
FT   DISULFID     128   153       By similarity.
FT   CARBOHYD     146   146       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC     135   241       TQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAA
FT                                CVLLLTSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDAR
FT                                SCQFPEEERGERSAEEKGRLGDLWV -> CWRCRRRPKTPE
FT                                AASSPRKSGASDRQRRRGGWETCGCEPGRPPGPPTAASPSP
FT                                GAPQAAGALRSALGRALLPWQQKWVQEGGSDQRPGPCSSAA
FT                                AAGPCRRERETQSWPPSSLAGPDGVGS (in isoform
FT                                2).
FT                                /FTId=VSP_006508.
FT   CONFLICT     194   201       SQCMWPRE -> K (in Ref. 2).
SQ   SEQUENCE   241 AA;  26000 MW;  90DC3B4AA7E82CBE CRC64;
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  Query Match           56.5%;  Score 735.5;  DB 1;  Length 241;
  Best Local Similarity  57.0%;  Pred. No. 1.9e-56;
  Matches  134;  Conservative   31;  Mismatches   61;  Indels    9;  Gaps    3;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-------PGKE 53
              |||:  | |:::|| | |||       ||||||::  |:| : ||| ::        ||:|
Db          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65

Qy         54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
                | :  |:|| ||:|||||  |  |:|:|| ||| |:|||   |||:|: || |||| | :
Db         66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125

Qy        114 GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
              |||: ||:|:||||||:|||||||||||:|   | |  | |||: | :|||:  ||: ||
Db        126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQL 185

Qy        174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEKCHLGGRW 227
              |||||||| | | |||||   ||  | ||| | |||||||||:: |||  ||  |
Db        186 GLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
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RESULT 4
TNR9_HUMAN
ID   TNR9_HUMAN     STANDARD;      PRT;   255 AA.
AC   Q07011;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   25-JAN-2005 (Rel. 46, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB
DE   ligand receptor) (T-cell antigen 4-1BB homolog) (T-cell antigen ILA)
DE   (CD137 antigen).
GN   Name=TNFRSF9; Synonyms=CD137, ILA;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=94374434; PubMed=8088337;
RA   Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J.,
RA   Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G.;
RT   "Molecular and biological characterization of human 4-1BB and its
RT   ligand.";
RL   Eur. J. Immunol. 24:2219-2227(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=94085794; PubMed=8262389; DOI=10.1016/0378-1119(93)90110-O;
RA   Schwarz H., Tuckwell J., Lotz M.;
RT   "A receptor induced by lymphocyte activation (ILA): a new member of
RT   the human nerve-growth-factor/tumor-necrosis-factor receptor family.";
RL   Gene 134:295-298(1993).
RN   [3]
RP   REVISION TO 107.
RA   Schwarz H.;
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=95347766; PubMed=7622190; DOI=10.1016/0165-2478(94)00227-I;
RA   Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E.,
RA   Kwon B.S.;
RT   "Characterization of human homologue of 4-1BB and its ligand.";
RL   Immunol. Lett. 45:67-73(1995).
RN   [5]
RP   SEQUENCE FROM N.A., AND VARIANTS THR-56; ASN-115 AND ASP-176.
RA   Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,
RA   Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA   Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RT   "NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department
RT   of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL   Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
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RN   [6]
RP   SEQUENCE FROM N.A.
RA   Pearce A.;
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [8]
RP   SEQUENCE OF 24-38.
RX   PubMed=15340161; DOI=10.1110/ps.04682504;
RA   Zhang Z., Henzel W.J.;
RT   "Signal peptide prediction based on analysis of experimentally
RT   verified cleavage sites.";
RL   Protein Sci. 13:2819-2824(2004).
RN   [9]
RP   INTERACTIONS WITH TRAF1; TRAF2 AND TRAF3.
RX   MEDLINE=98078711; PubMed=9418902;
RA   Arch R.H., Thompson C.B.;
RT   "4-1BB and Ox40 are members of a tumor necrosis factor (TNF)-nerve
RT   growth factor receptor subfamily that bind TNF receptor-associated
RT   factors and activate nuclear factor kappaB.";
RL   Mol. Cell. Biol. 18:558-565(1998).
RN   [10]
RP   INTERACTIONS WITH TRAF1 AND TRAF2.
RX   MEDLINE=98270914; PubMed=9607925;
RA   Saoulli K., Lee S.Y., Cannons J.L., Yeh W.C., Santana A.,
RA   Goldstein M.D., Bangia N., DeBenedette M.A., Mak T.W., Choi Y.,
RA   Watts T.H.;
RT   "CD28-independent, TRAF2-dependent costimulation of resting T cells by
RT   4-1BB ligand.";
RL   J. Exp. Med. 187:1849-1862(1998).
RN   [11]
RP   INTERACTION WITH LRR-REPEAT PROTEIN 1/LRR-1.
RX   MEDLINE=21662677; PubMed=11804328;
RA   Jang I.-K., Lee Z.-H., Kim H.-H., Hill J.M., Kim J.-D., Kwon B.S.;
RT   "A novel leucine-rich repeat protein (LRR-1): potential involvement in
RT   4-1BB-mediated signal transduction.";
RL   Mol. Cells 12:304-312(2001).
CC   -!- FUNCTION: Receptor for TNFSF14/4-1BBL. Possibly active during T
CC       cell activation.
CC   -!- SUBUNIT: Interacts with TRAF1, TRAF2 and TRAF3. Interacts with
CC       LRR-repeat protein 1/LRR-1.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed on the surface of activated T cells.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CDw137 entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdw137.htm".
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U03397; AAA53133.1; -.
DR   EMBL; L12964; AAA62478.2; -.
DR   EMBL; AY438976; AAR05440.1; -.
DR   EMBL; AL009183; CAB57398.1; -.
DR   EMBL; BC006196; AAH06196.1; -.
DR   PIR; I38426; I38426.
DR   HSSP; Q92956; 1JMA.
DR   Genew; HGNC:11924; TNFRSF9.
DR   H-InvDB; HIX0000096; -.
DR   MIM; 602250; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0004872; F:receptor activity; TAS.
DR   GO; GO:0006917; P:induction of apoptosis; TAS.
DR   GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Direct protein sequencing; Glycoprotein; Polymorphism; Receptor;
KW   Repeat; Signal; Transmembrane.
FT   SIGNAL       1     23
FT   CHAIN       24    255       Tumor necrosis factor receptor
FT                               superfamily member 9.
FT   DOMAIN      24    186       Extracellular (Potential).
FT   TRANSMEM   187    213       Potential.
FT   DOMAIN     214    255       Cytoplasmic (Potential).
FT   REPEAT      24     45       TNFR-Cys 1.
FT   REPEAT      47     86       TNFR-Cys 2.
FT   REPEAT      87    118       TNFR-Cys 3.
FT   REPEAT     119    159       TNFR-Cys 4.
FT   DOMAIN     214    255       Interaction with LRR-1.
FT   DISULFID    28     37       By similarity.
FT   DISULFID    31     45       By similarity.
FT   DISULFID    48     62       By similarity.
FT   DISULFID    65     78       By similarity.
FT   DISULFID    68     86       By similarity.
FT   DISULFID    88     94       By similarity.
FT   DISULFID    99    106       By similarity.
FT   DISULFID   102    117       By similarity.
FT   DISULFID   121    133       By similarity.
FT   DISULFID   139    158       By similarity.
FT   CARBOHYD   138    138       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   149    149       N-linked (GlcNAc. . .) (Potential).
FT   VARIANT     56     56       A -> T.
FT                               /FTId=VAR_018920.
FT   VARIANT    115    115       K -> N.
FT                               /FTId=VAR_018921.
FT   VARIANT    176    176       A -> D.
FT                               /FTId=VAR_018922.
SQ   SEQUENCE   255 AA;  27899 MW;  F3A563FE5EF00460 CRC64;

  Query Match             17.6%;  Score 228.5;  DB 1;  Length 255;
  Best Local Similarity   27.2%;  Pred. No. 5.2e-12;
  Matches   68;  Conservative   30;  Mismatches   97;  Indels   55;  Gaps   10;

Qy         11 SMLCVLDLGQPSVVEEP------------------GCGPGKVQNGSGNNT-----RCCS 46
              ::| ||:  :   :::|                  | |    :  | |     :|
Db         11 TLLLVLNFERTRSLQDPCSNCPAGTFCDNNRNQICSPCPPNSFSSAGGQRTCDICRQCKG 70

Qy         47 LYAPGKE--DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACA 104
              ::   ||        | | || :||    | :|:   |: || :  :|       | |
Db         71 VFRTRKECSSTSNAECDC-TPGFHCLGAGCSMCEQ-DCKQGQELTKKG-------CKDCC 121

Qy        105 MGTFSAGRDGHCRLWTNCSQFGFLTMFPGNKTHNAVCIPE-------------PLPTEQY 151
              |||:  : | || |||||  |   :  | |  : || |                | |  :
Db        122 FGTFNDQKRGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGASSVTPPAPAREP 181

Qy        152 GHLTVIF-----LVMAACIFFLTTVQLGLHIWQLRRQHMCPRETQPFAE-VQLS-AEDAC 204
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                ||   |       |   | :| |  : |   : :  |: :     |||   || :  || |
Db        182 GHSPQIISFFLALTSTALLFLLFFLTLRFSVVKRGRKKLLYIFKQPFMRPVQTTQEEDGC 241

Qy        205 SFQFPEEERG 214
              | :|||| |
Db        242 SCRFPEEEEG 251


RESULT 5
TNR9_MOUSE
ID   TNR9_MOUSE     STANDARD;      PRT;   256 AA.
AC   P20334;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB
DE   ligand receptor) (T-cell antigen 4-1BB) (CD137 antigen).
GN   Name=Tnfrsf9; Synonyms=Cd137, Cd157, ILA, Ly63;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89184547; PubMed=2784565;
RA   Kwon B.S., Weissman S.M.;
RT   "cDNA sequences of two inducible T-cell genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   MEDLINE=94179805; PubMed=8133039;
RA   Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.;
RT   "Genomic organization and chromosomal localization of the T-cell
RT   antigen 4-1BB.";
RL   J. Immunol. 152:2256-2262(1994).
RN   [3]
RP   CHARACTERIZATION, AND SEQUENCE OF 24-29.
RX   MEDLINE=93139510; PubMed=7678621;
RA   Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kin K.K., Pickard R.T.,
RA   Kwon B.S.;
RT   "Inducible T cell antigen 4-1BB. Analysis of expression and
RT   function.";
RL   J. Immunol. 150:771-781(1993).
CC   -!- FUNCTION: Receptor for TNFSF14/4-1BBL. Possibly active during T
CC       cell activation.
CC   -!- SUBUNIT: Principally an homodimer, but also found as a monomer.
CC       Associates with p56-LCK. Interacts with TRAF1, TRAF2 and TRAF3 (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed on the surface of activated T cells.
CC   -!- INDUCTION: Optimal by PMA and ionomycin.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; J04492; AAA40167.1; -.
DR   EMBL; U02567; AAA93113.1; -.
DR   PIR; B32393; B32393.
DR   PDB; 1D0J; X-ray; G/H/I/J/K=230-236.
DR   MGD; MGI:1101059; Tnfrsf9.
DR   InterPro; IPR009030; Grow_fac_recept.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
KW   3D-structure; Direct protein sequencing; Glycoprotein; Receptor;
KW   Repeat; Signal; Transmembrane.
FT   SIGNAL        1     23
FT   CHAIN        24    256       Tumor necrosis factor receptor
FT                                 superfamily member 9.
FT   DOMAIN       24    187       Extracellular (Potential).
FT   TRANSMEM    188    208       Potential.
FT   DOMAIN      209    256       Cytoplasmic (Potential).
FT   REPEAT       24     45       TNFR-Cys 1.
FT   REPEAT       46     85       TNFR-Cys 2.
FT   REPEAT       86    117       TNFR-Cys 3.
FT   REPEAT      118    159       TNFR-Cys 4.
FT   DISULFID     28     37       By similarity.
FT   DISULFID     31     44       By similarity.
FT   DISULFID     47     61       By similarity.
FT   DISULFID     64     77       By similarity.
FT   DISULFID     67     85       By similarity.
FT   DISULFID     87     93       By similarity.
FT   DISULFID     98    105       By similarity.
FT   DISULFID    101    116       By similarity.
FT   DISULFID    119    133       By similarity.
FT   DISULFID    139    158       By similarity.
FT   CARBOHYD    128    128       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    138    138       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   256 AA;  27598 MW;  93A10D03C60813C4 CRC64;

  Query Match             15.6%;  Score 203.5;  DB 1;  Length 256;
  Best Local Similarity   29.8%;  Pred. No. 8.1e-10;
  Matches   64;  Conservative   26;  Mismatches   84;  Indels   41;  Gaps   10;

Qy         22 SVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCP---KERCICVTPEYHCGDPQCKICK 78
              |:  :| |             | | |: |    |: |       | |:   :||  |||  |:
Db         54 SIGGQPNC----------NICRVCAGYFRFKKFCSSTHNAECECI-EGFHCLGPQCTRCE 102

Qy         79 HYPCQPGQRVESQGDIVFGFRCVACAMGTFS-AGRDGHCRLWTNCSQFGFLTMFPGNKTH 137
                |:||| :  ||        |  |:|||:     | || |||||  |   :  |
Db        103 K-DCRPGQELTKQG-------CKTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEK 154

Qy        138 NAVCIP-----EPLPTEQY-------GH----LTVIFLVMAACIFFLTTVQLGLHIWQLR 181
              : || |       | |           ||    ||:   : :| :  |  : |   : :
Db        155 DVVCGPPVVSFSPSTTISVTPEGGPGGHSLQVLTLFLALTSALLLALIFITLLFSVLKWI 214

Qy        182 RQHMCPRETQPFAEVQLSA--EDACSFQFPEEERG 214
              |:       ||| :   :|  ||||| : |:|| |
Db        215 RKKFPHIFKQPFKKTTGAAQEEDACSCRCPQEEEG 249


RESULT 6
Q8R037
ID   Q8R037      PRELIMINARY;      PRT;   211 AA.
AC   Q8R037;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Tnfrsf9 protein.
GN   Name=Tnfrsf9;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Uterus;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Uterus;
RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC028507; AAH28507.1; -.
DR   HSSP; Q92956; 1JMA.
DR   MGD; MGI:1101059; Tnfrsf9.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   InterPro; IPR011061; Antihaemostatic.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
SQ   SEQUENCE   211 AA;  22452 MW;  1EECA84EA32A8D50 CRC64;

  Query Match           14.1%;  Score 184;  DB 2;  Length 211;
  Best Local Similarity  28.1%;  Pred. No. 3.4e-08;
  Matches   56;  Conservative   20;  Mismatches   69;  Indels   54;  Gaps    9;

Qy         22 SVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCP---KERCICVTPEYHCGDPQCKICK 78
              |:  :| |           |  | |: |   |: |       | |:   :||  |||  |:
Db         54 SIGGQPNC----------NICRVCAGYFRPKKFCSSTHNAECECI-EGFHCLGPQCTRCE 102

Qy         79 HYPCQPGQRVESQGDIVFGFRCVACAMGTFS-AGRDGHCRLWTNCSQFGFLTMFPGNKTH 137
                |:||| :  ||       |  |::|||:     | || |||||  |   :  |
Db        103 K-DCRPGQELTKQG-------CKTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEK 154

Qy        138 NAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQLRRQHMCPRETQPFAEVQ 197
              : || |   |   :  | |                      : |     | :
Db        155 DVVCGP---PVVSFSPSTTI------------------------SVTPEGGPAFKKTT 185

Qy        198 LSA--EDACSFQFPEEERG 214
               :|  ||||| : |:|| |
Db        186 GAAQEEDACSCRCPQEEEG 204


RESULT 7
Q9DDD2
ID   Q9DDD2      PRELIMINARY;      PRT;   276 AA.
AC   Q9DDD2;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   CD40-homologue.
GN   Name=TNFSF5;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Tregaskes C.A.;
RL   Thesis (2001), University of Reading, Reading, UNITED KINGDOM.
DR   EMBL; AJ293700; CAC20218.1; -.
DR   HSSP; Q92956; 1JMA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR   GO; GO:0006915; P:apoptosis; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR008063; Fas_receptor.
DR   InterPro; IPR001005; Myb_DNA_binding.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   PRINTS; PR01680; FASRECEPTOR.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00037; MYB_1; UNKNOWN_1.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
SQ   SEQUENCE   276 AA;  30009 MW;  4040B7E0DB82454E CRC64;

  Query Match           13.5%;  Score 175;  DB 2;  Length 276;
  Best Local Similarity  23.5%;  Pred. No. 2.8e-07;
  Matches   67;  Conservative   34;  Mismatches   78;  Indels  106;  Gaps   16;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCG-PGKVQNGSG----NNTRCCSLYAPGKE-- 53
              ||   :|    :|| | |          ||| ||   | |     :  |||:   |||:
Db          1 MGRLGLL---GLLCALLL---------GCGQPGDAVNCSDKQYEHKGRCCNRCQPGKKLA 48

Qy         54 -DC--------------------------PKERC-----------------IC-VTPE 66
              :|                          | | |                 :|
Db         49 SECNDTEDSVCTPCENGQYQHSWTKERHCTPHEICEDNAGLIVKRHGNATHNTVCQCRAG 108

Qy         67 YHCGDPQCKIC-KHYPCQPGQRVESQGDIVFGF----------RCVACAMGTFS--AGR 112
              || |  |: | :: ||: |          |||           |  || ||||  : :
Db        109 MHCSDASCQTCVENEPCKQG----------FGFVAAMAEARMTSPCEPCAEGTFSNVSSK 158

Qy        113 DGHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQ 172
                | ||:| : | :     |  | : :|      : :   |:|:  : || :    |
Db        159 TEPCHFWTSCEEKGLVVKVKGTNTSDVIC-----ESSRRSSLSVLIPITAAVV----TCL 209

Qy        173 LGLHIW-----QLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEE 212
              :|: |:      |||:   |:: :  |  :|  :      || :|
Db        210 VGICIYCLVHTDLRRRG--PKQAEAEAPRELVTQQPEEVDFPVQE 252


RESULT 8
Q80WM9
ID   Q80WM9      PRELIMINARY;      PRT;   275 AA.
AC   Q80WM9;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 14 precursor.
GN   Name=Tnfrsf14;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Thymus;
RA   Benencia F., Conejo-Garcia J.R., Courreges M.C., Coukos G.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY264405; AAO89081.1; -.
DR   HSSP; Q92956; 1JMA.
DR   MGD; MGI:2675303; Tnfrsf14.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR   GO; GO:0006915; P:apoptosis; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR008063; Fas_receptor.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   PRINTS; PR01680; FASRECEPTOR.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor; Signal.
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FT   SIGNAL        1     38       Potential.
SQ   SEQUENCE   275 AA;  30171 MW;  C4A7EAD8EFC0521D CRC64;

  Query Match             11.8%;  Score 154;  DB 2;  Length 275;
  Best Local Similarity   27.7%;  Pred. No. 1.9e-05;
  Matches   66;  Conservative   28;  Mismatches   92;  Indels   52;  Gaps   17;

Qy          8 YGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRC--CSLYAPGK-----EDCPKER- 59
              | |  :|    |     | | | |       :   ::|  | :  |        ::|   :
Db         61 YHVKQVCSEHTG---TVCAP-CPPQTYTAHANGLSKCLPCGVCDPDMGLLTWQECSSWKD 116

Qy         60 --CICVTPEYHCGD---PQCKIC-KHYPCQPGQRVESQG----DIVFGFRCVACAMGTFS 109
                | |: | | | :     |  | :|  | |||||| :|    | |     |  |  ||||
Db        117 TVCRCI-PGYFCENQDGSHCSTCLQHTTCPPGQRVEKRGTHDQDTV----CADCLTGTFS 171

Qy        110 -AGRDGHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTV-----IFLVMAA 163
               |    | ||||| |    :  |  : :  |       : |  :  |      : :| |
Db        172 LGGTQEECLPWTNCSAFQ-QEVRRGTNSTDTTC------SSQVVYYVVSILLPLVIVGAG 224

Qy        164 CIFFLTTVQLGLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERG-EQTEEK 220
                ||   :  ||   :       :| :|| | | :     : :||  | |  :|||:
Db        225 IAGFLICTRRHLHTSSV------AKELEPFQEQQEN-----TIRFPVTEVGFAETEEE 271


RESULT 9
Q71F55
ID   Q71F55      PRELIMINARY;      PRT;   276 AA.
AC   Q71F55;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Herpes virus entry mediator.
GN   Name=Hvem;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvJ;
RA   Rickert S., Granger S.W., Ko M., Shukla D., Spear P.G., Kronenberg M.,
RA   Ware C.F.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF515707; AAQ08183.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR   GO; GO:0006915; P:apoptosis; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR008063; Fas_receptor.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   PRINTS; PR01680; FASRECEPTOR.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
SQ   SEQUENCE   276 AA;  30327 MW;  4A615FB2629E9125 CRC64;

  Query Match             11.5%;  Score 149.5;  DB 2;  Length 276;
  Best Local Similarity   26.9%;  Pred. No. 4.7e-05;
  Matches   64;  Conservative   34;  Mismatches   89;  Indels   51;  Gaps   18;

Qy          8 YGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRC--CSLYAPGK-----EDCPKER- 59
              | |  :|    |     | | | |       :   ::|  | :  |        ::|   :
Db         61 YHVKQVCSEHTG---TVCAP-CPPQTYTAHANGLSKCLPCGVCDPDMGLLTWQECSSWKD 116

Qy         60 --CICVTPEYHCGD---PQCKIC-KHYPCQPGQRVESQG----DIVFGFRCVACAMGTFS 109
                | |: | | | :     |  | :|  | |||||| :|    | |     |  |  ||||
Db        117 TVCRCI-PGYFCENQDGSHCSTCLQHTTCPPGQRVEKRGTHDQDTV----CADCLTGTFS 171

Qy        110 -AGRDGHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFL 168
               |    | |||| |    :  |  : :  |  :           |:: |: : :  |
Db        172 LGGTQEECLPWTNCSAFQ-QEVRRGTNSTDTTCSSQ----------VVYYVV-SILLPL 218

Qy        169 TTVQLGLHIWQL-RRQHM----CPRETQPFAEVQLSAEDACSFQFPEEERG-EQTEEK 220
                | :|:  : :  |:|:      :| :|| : |       : :||  | |  :|||:
Db        219 VIVGVGIAGFLICTRRHLHTSSVAKELEPFQQEQ----QENTIRFPVTEVGFAETEEE 272


RESULT 10
Q8VC17
ID   Q8VC17      PRELIMINARY;      PRT;   196 AA.
AC   Q8VC17;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Tnfrsf14 protein (Fragment).
GN   Name=Tnfrsf14;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Liver;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Liver;
RA   Strausberg R.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC022125; AAH22125.1; -.
DR   HSSP; Q92956; 1JMA.
DR   MGD; MGI:2675303; Tnfrsf14.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR   GO; GO:0006915; P:apoptosis; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   PRINTS; PR01680; FASRECEPTOR.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   196 AA;  21555 MW;  2AB3FF8905E260E8 CRC64;

  Query Match             11.2%;  Score 145.5;  DB 2;  Length 196;
  Best Local Similarity   29.5%;  Pred. No. 7.5e-05;
  Matches   52;  Conservative   26;  Mismatches   61;  Indels   37;  Gaps   13;

Qy         60 CICVTPEYHCGD---PQCKIC-KHYPCQPGQRVESQG----DIVFGFRCVACAMGTFS-A 110
                | |: | | | :     |  | :|  | |||||| :|    | |     |  |  ||||
Db         39 CRCI-PGYFCENQDGSHCSTCLQHTTCPPGQRVEKRGTHDQDTV----CADCLTGTFSLG 93

Qy        111 GRDGHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTT 170
               |    | |||| |    :  |  : :  |  :           |:: |: : :  |
```

```
Db         94 GTQEECLPWTNCSAFQ-QEVRRGTNSTDTTCSSQ----------VVYYVV-SILLPLVI 140

Qy        171 VQLGLHIWQL-RRQHM----CPRETQPFAEVQLSAEDACSFQFPEEERG-EQTEEK 220
              | :|:  : :  |:|:      :| :|| : |       : :||  | |  :|||:
Db        141 VGVGIAGFLICTRRHLHTSSVAKELEPFQQEQ----QENTIRFPVTEVGFAETEEE 192


RESULT 11
Q7T2H3
ID   Q7T2H3      PRELIMINARY;      PRT;   318 AA.
AC   Q7T2H3;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Tumour necrosis factor receptor.
GN   Name=tnfr;
OS   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8022;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Head kidney;
RA   Zou J., Secombes C.J.;
RL   Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ517804; CAD57165.1; -.
DR   HSSP; Q92956; 1JMA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS01186; EGF_2; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 4.
KW   Receptor.
SQ   SEQUENCE   318 AA;  35254 MW;  78F8135011283B43 CRC64;

  Query Match             10.7%;  Score 139;  DB 2;  Length 318;
  Best Local Similarity   23.7%;  Pred. No. 0.00045;
  Matches   50;  Conservative   28;  Mismatches   91;  Indels   42;  Gaps    9;

Qy         29 CGPGKVQNGSGNN--TRCCSLYAPGKEDCPKERCICVTPEYHCGDPQCKICKHYP-CQPG 85
              | | :|   | |    | |       |     :|:| |  |:| |  |: |    | |
Db         61 CLPCRVCYSSSNQKVLREC-------EASSDRQCVCKT-GYYCTDDGCEHCLPVTLCPLG 112

Qy         86 QRVESQGDIVFGFRCVACAMGTFSAGRDG--HCRLWTNCSQFGFLTMFPGNKTHNAVC-- 141
                | :| :      |  |  ||:::  |   ||:  | |   |      | :| :|||
Db        113 SGVVNQANPQNDTVCAPCQPGTYNSFNDAFTHCQSHTRCGDLGKEVKSAGTETTDAVCGA 172

Qy        142 ----IPEPLPTEQYGHLTVI-FLVMAACIFFLTTVQLGLHIWQLRRQHMCPRET------ 190
                   |||  :  | |   :::  ||:          |: :||   |  :
Db        173 FISRCHWILPTSLWAGLVVTSLIIILICIY----------WRAKRQSYMPANSSSPGIP 221

Qy        191 -----QPFAEVQLSAEDACSFQFPEEERGEQ 216
                  ||  :|     |:  :  :::  :
Db        222 VEPAPSSFAPAELKFPTECNSHWSLDQKATE 252


RESULT 12
Q75SV8
ID   Q75SV8      PRELIMINARY;      PRT;   270 AA.
AC   Q75SV8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   CD134 homologue.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Shimojima M., Miyazawa T., Ikeda Y., McMonagle E.L., Haining H.,
RA   Akashi H., Takeuchi Y., Hosie M.J., Willett B.J.;
RT   "Use of CD134 as a primary receptor by the feline immunodeficiency
RT   virus.";
RL   Science 0:0-0(2004).
DR   EMBL; AB128982; BAD11363.1; -.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ   SEQUENCE   270 AA;  28731 MW;  36A40BAD261140D1 CRC64;

  Query Match             10.6%;  Score 138.5;  DB 2;  Length 270;
  Best Local Similarity   26.3%;  Pred. No. 0.00042;
  Matches   59;  Conservative   18;  Mismatches   72;  Indels   75;  Gaps   12;

Qy         29 CGPGKVQNGSGNNTRC-------CSLYAPG-------KEDC-------------PKERCI 61
              | |      | |  :||        |   | |         | |              ||:||
Db         47 CPP-----GYGMESRCSGDQDTKCLQCASGFYNEAVNYEPCKPCTQCNQRSGSEPKQRC- 100

Qy         62 CVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWTN 121
                ||       |  :|:   |:||   | |       |  | |  | || | |   |: |||
Db        101 --TP------TQDTVCR---CRPG--TEPQDGYDRGVDCAPCPPGHFSPGDDQACKPWTN 147

Qy        122 CSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQLR 181
              |:  |  |: | ::  :|||      |                        ||       |: :
Db        148 CTLAGKRTLRPASQGSDAVCEDRSPPA-------------------TTP------WETQ 181

Qy        182 RQHMCPRETQPFAEVQLSAEDACSFQFP-EEERGEQTEEKCHLG 224
                : |  |||      ::::   |  | |  || |      ||
Db        182 GPPVRPPTTQPTTAWPRTSQE--PFTPPAEPPRGPQLAAVLGLG 223


RESULT 13
Q76LB4
ID   Q76LB4      PRELIMINARY;      PRT;   290 AA.
AC   Q76LB4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   CD40.
GN   Name=CD40;
OS   Paralichthys olivaceus (Japanese flounder).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC   Pleuronectoidei; Paralichthyidae; Paralichthys.
OX   NCBI_TaxID=8255;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Park C., Hirono I., Aoki T.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Park C., Hirono I., Aoki T.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB081752; BAC87848.1; -.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR001368; TNFR_c6.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
SQ   SEQUENCE   290 AA;  32396 MW;  B6FCF9E35305DFAA CRC64;

  Query Match             10.6%;  Score 137.5;  DB 2;  Length 290;
  Best Local Similarity   22.9%;  Pred. No. 0.00056;
  Matches   46;  Conservative   28;  Mismatches   74;  Indels   53;  Gaps   11;

Qy         26 EPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERCICVTPEYHCGDPQCKIC-KHYPCQP 84
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           :| | | |       | |     :  |:      |||:   :||    |  |  |  |:|
Db         78 QPYCDPNK-------NLRVTKPESKTKQ----SPCICLL-GFHCSSGTCVTCVPHATCKP 125

Qy         85 GQRVESQGDIVFGFRCVACAMGTFSAGR--DGHCRLWTNCSQFGFLTMFPGNKTHNAVCI 142
              ||  : :|::     | :|  |:||        |  || | : |:     |    : :|:
Db        126 GQWAKIKGNLTHDTVCESCPEGSFSTSHSWSSVCTKWTEC-ESGYHIQESGTNESDNICV 184

Qy        143 PEPLPTEQYGHLTVIFLVMAACIFFLTTVQ-LGLHIWQLRRQHMCPRETQPFAEVQLSAE 201
                  |   :| |         ||:  : ::  :|| :       :|  ||
Db        185 E---PPRHHGGL-------IACVVAVGSLAVVGLMVC------LCKGET---------- 217

Qy        202 DACSFQFPEEERGEQTEEKCH 222
                    ::| :   | ||
Db        218 ---------KQRAKDYLESCH 229


RESULT 14
Q6PI12
ID   Q6PI12      PRELIMINARY;      PRT;   401 AA.
AC   Q6PI12;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Tumor necrosis factor receptor superfamily, member 11b
DE   (Osteoprotegerin).
GN   Name=Tnfrsf11b;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Limb;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Limb;
RA   Strausberg R.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC049782; AAH49782.1; -.
DR   GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IDA.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0042489; P:negative regulation of odontogenesis (sensu. . .; IDA.
DR   InterPro; IPR000488; Death.
DR   InterPro; IPR011029; DEATH_like.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00005; DEATH; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS50017; DEATH_DOMAIN; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Receptor.
```

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SQ   SEQUENCE   401 AA;  45965 MW;  7C708E52EB46BA0E CRC64;

  Query Match             10.5%;  Score 136;  DB 2;  Length 401;
  Best Local Similarity   28.2%;  Pred. No. 0.001;
  Matches   44;  Conservative   10;  Mismatches   54;  Indels   48;  Gaps    7;

Qy         45 CSLYAPG---KEDCP-KERCICV-------TPEYHCGD------PQCK------------ 75
              | |||    |: |  : : :||       |  :|  |      | |||
Db         41 CDKCAPGTYLKQHCTVRRKTLCVPCPDHSYTDSWHTSDECVYCSPVCKELQSVKQECNRT 100

Qy         76 ---IC-------------KHYPCQPGQRVESQGDIVFGFRCVACAMGTFS--AGRDGHC 116
                 :|             ||  | ||  |   |       |  |  | ||       |
Db        101 HNRVCECEEGRYLEIEFCLKHRSCPPGSGVVQAGTPEQNTVCKKCPDGFFSGETSSKAPC 160

Qy        117 RLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYG 152
              |  |||| || | :  || ||: ||      |:: |
Db        161 RKHTNCSTFGLLLIQKGNATHDNVCSGNREATQKCG 196


RESULT 15
Q800I0
ID   Q800I0      PRELIMINARY;      PRT;   467 AA.
AC   Q800I0;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   CD30 protein precursor.
GN   Name=CD30;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=15356338;
RA   Burgess S.C., Young J.R., Baaten B.J.G., Hunt L., Ross L.N.J.,
RA   Parcells M.S., Kumar M.S., Tregaskes C.A., Lee L.F., Davison T.F.;
RT   "Marek's disease is a natural model for lymphomas overexpressing
RT   Hodgkin's disease antigen (CD30).";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:13879-13884(2004).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Burgess S.C.;
RL   Thesis (1998), Bristol University, UK.
DR   EMBL; AJ276964; CAC79223.1; -.
DR   HSSP; Q92956; 1JMA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0005031; F:tumor necrosis factor receptor activity; IEA.
DR   GO; GO:0019221; P:cytokine and chemokine mediated signaling p. . .; IEA.
DR   InterPro; IPR011366; TNFrecept_2.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 1.
DR   PIRSF; PIRSF001968; TNFR_2; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Signal.
FT   SIGNAL        1     21       Potential.
FT   CHAIN        22    467       CD30 protein.
SQ   SEQUENCE   467 AA;  51350 MW;  F9AD4F77DEEC8588 CRC64;

  Query Match             10.4%;  Score 135.5;  DB 2;  Length 467;
  Best Local Similarity   21.1%;  Pred. No. 0.0013;
  Matches   71;  Conservative   33;  Mismatches   95;  Indels  137;  Gaps   18;

Qy          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNT--RCC----SLYAPGK-- 52
              :| | :|    :  :    ||       |    ::|   : |  |||    | ||  |
Db          8 LGLWLLLL---LQDIQGAPQPPFTSSHSC--DTLKNWFYDETLGRCCYQCPSGYAKKKSC 62

Qy         53 -----EDC-----------PKERC-ICV--TPEYH------CGDPQCKIC--------- 77
                  |||           || ||  ||  | |:       |     ::|
```

```
Db         63 PMDPDEDCMRCGPEQYLNQSPKPRCDACVLCTKEFDLVEKAPCSFNSSRVCECRPGMFCQ 122

Qy         78 ----------KHYPCQPGQRVESQGDIVFGFRCVACAMGTFS--AGRDGHCRLWTNCSQ 124
                      :|  .|:||  |: :|       |  |  ||||  :     |:  |:|::
Db        123 TAAKNTCMRCQRHTACKPGFGVKIRGTSETDVSCEECPPGTFSDQSSSTDVCKPHTDCAK 182

Qy        125 FGFLTMFPGNKTHNAVC---------------------------------------------- 141
               :    || ||: ||
Db        183 LNKVAQGKGNATHDQVCTDQLPSYLTPDTSSIRITNETDDSDVLKRNANPVTLASILSSA 242

Qy        142 ---IPEPLPTEQ----------YGHLTVIFLVMAACIFFLTTVQLG-LHIWQLRRQHMCP 187
                 ||   | |:          |  |   ||  | :  :  : :| |  || :   :|
Db        243 TTEIPGSTPEEEALAGTSPTLAKGETTTRGLVFWAVVLSVMVLPVGMLSFWQWK---VCK 299

Qy        188 RE----------TQPFAEVQLSAEDACSFQFPEEE 212
               :              :|:: |:  | |    ||||
Db        300 KRIFILKQKRSDLVDKYAKITLTT-DKC----PEEE 330
```

Search completed: October 26, 2005, 15:51:38
Job time : 118.299 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 26, 2005, 15:28:42 ; Search time 141.311 Seconds
(without alignments)
659.602 Million cell updates/sec

Title: US-09-545-998B-4
Perfect score: 1386
Sequence: 1 MAQHGAMGAFRALCGLALLC.....EEERGERSAEEKGRLGDLWV 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1386	100.0	241	2	AAW37839	Aaw37839 Amino aci
2	1386	100.0	241	2	AAY06605	Aay06605 Human TNF
3	1386	100.0	241	3	AAB33431	Aab33431 Human PRO
4	1386	100.0	241	3	AAY71467	Aay71467 Human PRO
5	1386	100.0	241	3	AAB27651	Aab27651 Human pro
6	1386	100.0	241	3	AAY95895	Aay95895 Human tum
7	1386	100.0	241	3	AAB24409	Aab24409 Human PRO
8	1386	100.0	241	4	AAB47054	Aab47054 Human PRO
9	1386	100.0	241	4	AAB20115	Aab20115 Human imm
10	1386	100.0	241	4	AAB53090	Aab53090 Human ang
11	1386	100.0	241	4	AAB47289	Aab47289 PRO364 po
12	1386	100.0	241	4	AAB50982	Aab50982 Human PRO
13	1386	100.0	241	4	AAB50910	Aab50910 Human PRO
14	1386	100.0	241	5	AAE28161	Aae28161 Human TR1
15	1386	100.0	241	6	ABU08442	Abu08442 Amino aci
16	1386	100.0	241	6	AAO16574	Aao16574 Human tum
17	1386	100.0	241	6	AAO23091	Aao23091 Human ene
18	1386	100.0	241	7	ADN39966	Adn39966 Cancer/an
19	1386	100.0	241	8	ADH43131	Adh43131 Human TNF
20	1386	100.0	241	8	ADL91869	Adl91869 Human PRO
21	1386	100.0	241	8	ADO20289	Ado20289 Human PRO
22	1386	100.0	241	8	ADP55559	Adp55559 Human PRO
23	1386	100.0	241	8	ADT94287	Adt94287 Human PRO
24	1382	99.7	240	8	ADR46662	Adr46662 Cancer-as
25	1347	97.2	235	3	AAY44825	Aay44825 Human mol
26	1347	97.2	235	6	AAO16576	Aao16576 Human tum
27	1347	97.2	235	6	AAO23093	Aao23093 Human ene
28	1322.5	95.4	234	3	AAY95879	Aay95879 Human tum
29	1322.5	95.4	234	3	AAY52158	Aay52158 Tumour ne
30	1322.5	95.4	234	5	AAE28158	Aae28158 Human TR1
31	1322.5	95.4	234	6	ABU08439	Abu08439 Amino aci
32	1322.5	95.4	234	6	AAO16575	Aao16575 Human tum
33	1322.5	95.4	234	6	ADA09435	Ada09435 Human TR1
34	1322.5	95.4	234	6	AAO23092	Aao23092 Human ene
35	1322.5	95.4	234	8	ADH43105	Adh43105 Human TNF
36	1322.5	95.4	234	8	ADO20305	Ado20305 Human PRO
37	1306.5	94.3	246	5	ABB89386	Abb89386 Human pol
38	1293.5	93.3	228	6	AAO23094	Aao23094 Human ene
39	1290.5	93.1	228	2	AAW37840	Aaw37840 Truncated
40	1290.5	93.1	228	6	AAO16577	Aao16577 Human tum
41	1290.5	93.1	228	6	AAO23099	Aao23099 Human ene
42	1274.5	92.0	240	3	AAY95881	Aay95881 Human tum
43	1274.5	92.0	240	3	AAY52160	Aay52160 TR11SV2 a
44	1274.5	92.0	240	5	AAE28160	Aae28160 Human TR1
45	1274.5	92.0	240	6	ABU08441	Abu08441 Amino aci

ALIGNMENTS

RESULT 1
AAW37839
ID AAW37839 standard; protein; 241 AA.
XX
AC AAW37839;
XX
DT 28-JUL-1998 (first entry)
XX
DE Amino acid sequence of the human 312C2 T cell protein.
XX
KW Human 312C2 T cell protein; thymus cell; spleen cell; T cell;
KW antigen-specific T cell proliferation; cytokine production by T-cell;
KW apoptosis; cancer; haematopoietic cells; lymphoid cell;
KW autoimmune disorders.
XX
OS Homo sapiens.
XX
PN WO9806842-A1.
XX
PD 19-FEB-1998.
XX
PF 14-AUG-1997; 97WO-US013931.
XX
PR 16-AUG-1996; 96US-00689943.
PR 07-OCT-1996; 96US-0027901P.
XX
PA (SCHE) SCHERING CORP.
XX
PI Gorman DM, Randall TD, Zlotnik A;
XX
DR WPI; 1998-159534/14.
DR N-PSDB; AAV19153.
XX
PT Isolated 312C2 T cell gene - used to develop products for treating, e.g.
PT cancers, auto-immune disorders, transplantation rejection and other T
PT cell disorders.
XX
PS Claim 2; Page 59-60; 71pp; English.
XX
CC This is the amino acid sequence encoding the human 312C2 T cell protein.
CC The 312C2 proteins are expressed in thymus cells and are induced on T
CC cells and spleen cells following activation. Engagement of 312C2
CC stimulates proliferation of T cell clones, antigen-specific proliferation
CC and cytokine production by T-cells, and potentiates T cell expansion or
CC apoptosis. The products can be used in the treatment of conditions
CC associated with abnormal physiology or development, including abnormal
CC proliferation, e.g. cancerous conditions or degenerative conditions. They
CC can be used in the regulation or development of haematopoietic cells,

```
CC   e.g. lymphoid cells which affect immunological responses, e.g. autoimmune
CC   disorders
XX
SQ   Sequence 241 AA;

  Query Match             100.0%;  Score 1386;  DB 2;  Length 241;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-101;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60

Qy         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120

Qy        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180

Qy        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240

Qy        241 V 241
              |
Db        241 V 241


RESULT 2
AAY06605
ID   AAY06605 standard; protein; 241 AA.
XX
AC   AAY06605;
XX
DT   26-OCT-1999  (first entry)
XX
DE   Human TNF receptor homologue PRO364.
XX
KW   PRO364; tumour necrosis factor receptor; human; apoptosis; inflammation;
KW   antiinflammatory; NF-KB activation; autoimmune disease; therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .25
FT                   /note= "signal peptide"
FT   Protein         26. .241
FT                   /note= "mature protein"
FT   Modified-site   146
FT                   /note= "N-glycosylated"
FT   Domain          162. .180
FT                   /note= "transmembrane domain"
XX
PN   WO9940196-A1.
XX
PD   12-AUG-1999.
XX
PF   09-FEB-1999;   99WO-US002642.
XX
PR   09-FEB-1998;   98US-0074087P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Gurney AL,  Marsters SA,  Pitti RM,  Wood WI;
PI   Goddard A;
XX
DR   WPI; 1999-494296/41.
DR   N-PSDB; AAX87670.
XX
PT   Tumor necrosis factor receptor homologue - useful for, e.g. modulating
PT   apoptosis and NF-KB activation and proinflammatory or autoimmune
PT   responses.
XX
PS   Claim 17; Fig 2A; 104pp; English.
XX
CC   The present sequence represents human PRO364, a novel member of the
CC   tumour necrosis factor receptor family. The sequence was deduced from a
CC   bone marrow cDNA clone (see AAX87670). Methods for the recombinant
CC   production of PRO364 polypeptides, e.g. in CHO, Escherichia coli or yeast
CC   host cells, are provided. Claimed polypeptides comprise amino acids 1-
CC   241, 1-X, 26-241 (i.e. the mature protein) and 26-X of the present
CC   sequence, where X is any one of amino acid respdies 157-167 of PRO364.
CC   PRO364 polypeptides are useful for modulating apoptosis, NF-KB activation
CC   and proinflammatory or autoimmune responses in mammalian cells (claimed).
CC   Chimeric molecules comprising a PRO364 polypeptide fused to a
CC   heterologous sequence such as epitope tag or immunoglobulin Fc region are
CC   also claimed. PRO364 can be used in assays to identify other proteins or
CC   molecules involved in binding interactions. This is useful for
CC   identifying inhibitors or agonists of receptor/ligand binding. The PRO364
CC   polypeptides may also be combined with an agent that is cytotoxic,
CC   chemotherapeutic or a growth inhibitor. PRO364 antibodies are useful in
CC   diagnostic methods, purification methods and also in therapy, e.g. as
CC   inhibitors
XX
SQ   Sequence 241 AA;

  Query Match             100.0%;  Score 1386;  DB 2;  Length 241;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-101;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60

Qy         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120

Qy        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180

Qy        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240

Qy        241 V 241
              |
Db        241 V 241


RESULT 3
AAB33431
ID   AAB33431 standard; protein; 241 AA.
XX
AC   AAB33431;
XX
DT   29-JAN-2001  (first entry)
XX
DE   Human PRO364 protein UNQ319 SEQ ID NO:92.
XX
KW   Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW   dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW   haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW   antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW   antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW   osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW   idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW   systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW   autoimmune thrombocytopaenia; immune-mediated renal disease;
KW   demyelinating disease; hepatobiliary disease; Whipple's disease;
KW   inflammatory bowel disease; gluten-sensitive enteropathy;
KW   autoimmune disease; immune-mediated skin disease; allergic disease;
KW   immunological disease; transplantation associated disease;
```

```
KW   graft rejection; graft-versus-host-disease.
XX
OS   Homo sapiens.
XX
PN   WO200053758-A2.
XX
PD   14-SEP-2000.
XX
PF   02-MAR-2000; 2000WO-US005841.
XX
PR   08-MAR-1999;   99WO-US005028.
PR   10-MAR-1999;   99US-0123618P.
PR   12-MAR-1999;   99US-0123957P.
PR   23-MAR-1999;   99US-0125775P.
PR   12-APR-1999;   99US-0128849P.
PR   20-APR-1999;   99WO-US008615.
PR   28-APR-1999;   99US-0131445P.
PR   04-MAY-1999;   99US-0132371P.
PR   14-MAY-1999;   99US-0134287P.
PR   02-JUN-1999;   99WO-US012252.
PR   23-JUN-1999;   99US-0141037P.
PR   20-JUL-1999;   99US-0144758P.
PR   26-JUL-1999;   99US-0145698P.
PR   28-JUL-1999;   99US-0146222P.
PR   01-SEP-1999;   99WO-US020111.
PR   08-SEP-1999;   99WO-US020594.
PR   13-SEP-1999;   99WO-US020944.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   05-OCT-1999;   99WO-US023089.
PR   29-OCT-1999;   99US-0162506P.
PR   29-NOV-1999;   99WO-US028214.
PR   30-NOV-1999;   99WO-US028313.
PR   30-NOV-1999;   99WO-US028409.
PR   01-DEC-1999;   99WO-US028301.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028564.
PR   02-DEC-1999;   99WO-US028565.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030999.
PR   30-DEC-1999;   99WO-US031274.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000277.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Goddard A,  Gurney AL,  Hebert C,  Henzel W;
PI   Kabakoff RC,  Lu Y,  Pan J,  Pennica D,  Shelton DL,  Smith V;
PI   Stewart TA,  Tumas D,  Watanabe CK,  Wood WI,  Yan M;
XX
DR   WPI; 2000-572271/53.
DR   N-PSDB; AAC58596.
XX
PT   Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT   immune related disorders, e.g. systemic lupus erythematosis, rheumatoid
PT   arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
XX
PS   Claim 33; Fig 36; 309pp; English.
XX
CC   The present invention describes sixty four human PRO proteins which can
CC   be used in the treatment of immune related diseases. The human PRO
CC   proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC   treating and diagnosing immune related disorders. The disorders are
CC   selected from systemic lupus erythematosus, rheumatoid arthritis,
CC   osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC   systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC   syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC   anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC   immune-mediated renal disease, demyelinating diseases of the central and
CC   peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
CC   disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
CC   or immune-mediated skin diseases, allergic diseases, immunological
CC   diseases of the lung, and transplantation associated diseases including
CC   graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
CC   represent PCR primers and hybridisation probes used in the isolation of
CC   human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
CC   represent human PRO polynucleotide and protein sequences given in the
CC   exemplification of the present invention
XX
SQ   Sequence 241 AA;

  Query Match             100.0%;  Score 1386;  DB 3;  Length 241;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-101;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60

Qy         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120

Qy        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180

Qy        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240

Qy        241 V 241
              |
Db        241 V 241


RESULT 4
AAY71467
ID   AAY71467 standard; protein; 241 AA.
XX
AC   AAY71467;
XX
DT   08-NOV-2000  (first entry)
XX
DE   Human PRO364 protein.
XX
KW   PRO364; DNA47365-1206; human; ATCC No: 209436; antiproliferative;
KW   neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour;
KW   breast; prostate; colon; lung; renal; ovarian; central nervous system;
KW   CNS; leukemia; melanoma; Expressed Sequence Tag; EST; TNFR homologue;
KW   tumour necrosis factor receptor; GITR protein homologue.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .25
FT                   /label= Signal_peptide
FT   Modified-site   5. .11
FT                   /note= "N-myristoylation site"
FT   Modified-site   8. .14
FT                   /note= "N-myristoylation site"
FT   Modified-site   25. .31
FT                   /note= "N-myristoylation site"
FT   Protein         26. .241
FT                   /label= Mature_PRO364_protein
FT   Modified-site   30. .36
FT                   /note= "N-myristoylation site"
FT   Modified-site   33. .39
FT                   /note= "N-myristoylation site"
FT   Modified-site   118. .124
```

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FT                  /note= "N-myristoylation site"
FT   Modified-site  122. .128
FT                  /note= "N-myristoylation site"
FT   Modified-site  146. .150
FT                  /note= "Asn is N-glycosylated"
FT   Modified-site  156. .162
FT                  /note= "N-myristoylation site"
FT   Domain         163. .183
FT                  /label= Transmembrane_domain
FT   Binding-site   166. .177
FT                  /note= "Prokaryotic membrane lipoprotein lipid attachment
FT                  site"
FT   Region         171. .193
FT                  /note= "Leucine zipper pattern"
XX
PN   WO200032778-A2.
XX
PD   08-JUN-2000.
XX
PF   30-NOV-1999;   99WO-US028409.
XX
PR   01-DEC-1998;   98WO-US025108.
PR   16-DEC-1998;   98US-0112850P.
PR   22-DEC-1998;   98US-0113296P.
PR   20-JUL-1999;   99US-0144758P.
PR   26-JUL-1999;   99US-0145698P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Chen J,  Goddard A,  Gurney AL,  Hillan K,  Napier M,  Wood WI;
XX
DR   WPI; 2000-412325/35.
DR   N-PSDB; AAD01240.
XX
PT   New composition useful for inhibiting neoplastic cell growth and for
PT   treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or their
PT   antagonists.
XX
PS   Claim 31; Fig 4; 108pp; English.
XX
CC   The present sequence is the human PRO364 protein, encoded by the cDNA
CC   clone, designated as DNA47365-1206. It is isolated from human small
CC   intestine tissue cDNA library, identified using probes based on the
CC   consensus sequence DNA44825, relative to the Incyte expressed sequence
CC   tag (EST) 3003460. This EST has homology to tumour necrosis factor
CC   receptor (TNFR) family of polypeptides. PRO364 sequence also shows
CC   homology to members of the TNFR family and mouse GITR protein. This clone
CC   is assigned the ATCC deposit No: 209436. PRO364 functions as a neoplastic
CC   cell growth inhibitor and is used for treating tumours, using an
CC   effective amount of PRO655, PRO364 and PRO344. This composition is
CC   especially useful for treatment of human cancers such as breast,
CC   prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma
XX
SQ   Sequence 241 AA;

  Query Match             100.0%;  Score 1386;  DB 3;  Length 241;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-101;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60

Qy         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120

Qy        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180

Qy        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240

Qy        241 V 241
              |
Db        241 V 241


RESULT 5
AAB27651
ID   AAB27651 standard; protein; 241 AA.
XX
AC   AAB27651;
XX
DT   26-JAN-2001  (first entry)
XX
DE   Human protein PRO364.
XX
KW   Cardiovascular; endothelial; angiogenic disorder; PRO179; PRO238; PRO364;
KW   PRO844; PRO846; PRO1760; PRO205; PRO321; PRO333; PRO840; PRO877; PRO878;
KW   PRO879; PRO882; PRO885; PRO887; gene therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .25
FT                   /label= Signal peptide
XX
PN   WO200053757-A2.
XX
PD   14-SEP-2000.
XX
PF   24-FEB-2000; 2000WO-US005004.
XX
PR   08-MAR-1999;   99WO-US005028.
PR   12-MAR-1999;   99US-0123957P.
PR   02-JUN-1999;   99WO-US012252.
PR   20-JUL-1999;   99US-0144758P.
PR   26-JUL-1999;   99US-0145698P.
PR   01-SEP-1999;   99WO-US020111.
PR   15-SEP-1999;   99WO-US021090.
PR   30-NOV-1999;   99WO-US028313.
PR   30-NOV-1999;   99WO-US028409.
PR   02-DEC-1999;   99WO-US028565.
PR   05-JAN-2000; 2000WO-US000219.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Ferrara N,  Gerber H,  Gerritsen ME;
PI   Goddard A,  Gurney AL,  Hillan KJ,  Marsters SA,  Paoni NF,  Pitti RM;
PI   Watanabe CK,  Williams PM,  Wood WI;
XX
DR   WPI; 2000-611444/58.
DR   N-PSDB; AAA99903.
XX
PT   Novel PRO polypeptides and agonists and antagonists of them, used to
PT   diagnose and treat cardiovascular, endothelial and angiogenic disorders.
XX
PS   Claim 71; Fig 6; 181pp; English.
XX
CC   The present invention relates to methods for stimulating or inhibiting
CC   angiogenesis and cardiovascularization. The methods involve the use of
CC   pharmaceutical compositions based on the following proteins, PRO179,
CC   PRO238, PRO364, PRO844, PRO846, PRO1760, PRO205, PRO321, PRO333, PRO840,
CC   PRO877, PRO878, PRO879, PRO882, PRO885 or PRO887. These proteins were
CC   identified by isolating cDNA clones encoding secreted proteins. The
CC   proteins of the invention may be used to diagnose and treat
CC   cardiovascular, endothelial or angiogenic disorders. The present sequence
CC   is one of the proteins of the invention
XX
SQ   Sequence 241 AA;
```

```
  Query Match             100.0%;  Score 1386;  DB 3;  Length 241;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-101;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60

Qy         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120

Qy        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180

Qy        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240

Qy        241 V 241
              |
Db        241 V 241


RESULT 6
AAY95895
ID   AAY95895 standard; protein; 241 AA.
XX
AC   AAY95895;
XX
DT   20-NOV-2000  (first entry)
XX
DE   Human tumour necrosis factor receptor-like protein TR11 mutein.
XX
KW   TR11; human; tumour necrosis factor receptor-like protein;
KW   immunodeficiency; autoimmune disease; rheumatoid arthritis;
KW   immunosuppressive; antirheumatic; antiarthritic; haemostatic;
KW   dermatological; antiinflammatory; therapy; diagnosis; mutein; mutant.
XX
OS   Homo sapiens.
XX
PN   WO200050459-A1.
XX
PD   31-AUG-2000.
XX
PF   23-FEB-2000; 2000WO-US004572.
XX
PR   24-FEB-1999;   99US-0121648P.
PR   13-MAY-1999;   99US-0134172P.
PR   16-JUL-1999;   99US-0144076P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM,  Ni J;
XX
DR   WPI; 2000-572072/53.
XX
PT   Human tumor necrosis factor receptor-like proteins useful for diagnosis,
PT   prevention and treatment of disease states associated with aberrant cell
PT   survival such as autoimmune disease and rheumatoid arthritis.
XX
PS   Disclosure; 294-295; 278pp; English.
XX
CC   The present sequence is that of human tumour necrosis factor receptor-
CC   like protein TR11 (see also AAY95879), a novel protein showing identity
CC   to murine glucocorticoid induced tumour necrosis factor receptor family-
CC   related gene. The invention provides highly conserved TR11, TR11SV1 and
CC   TR11SV2 proteins (see AAY95879-81), as well as vectors, host cells and
CC   recombinant methods for their production. TR11, TR11SV1 and/or TR11SV2
CC   polypeptides are useful for treating, preventing, prognosis and/or
CC   diagnosis of an immunodeficiency, especially common variable
CC   immunodeficiency, X-linked agammaglobulinemia, severe combined
CC   immunodeficiency (SCID), Wiskott-Aldrich syndrome or X-linked
CC   immunoglobulin deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2
CC   antagonists (e.g. antibodies) are used to treat, prevent, prognose and/or
CC   diagnose an autoimmune disease, especially rheumatoid arthritis, systemic
CC   lupus erythematosus, thrombocytopenia purpura or IgA nephropathy. The
CC   polypeptides, polynucleotides and/or antibodies can be administered to
CC   cells in vitro, ex vivo or in vivo or to a multicellular organism.
CC   Soluble forms of the polypeptides may also be used. Methods for screening
CC   for agonist/antagonist compounds are also provided
XX
SQ   Sequence 241 AA;

  Query Match             100.0%;  Score 1386;  DB 3;  Length 241;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-101;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60

Qy         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120

Qy        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180

Qy        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240

Qy        241 V 241
              |
Db        241 V 241


RESULT 7
AAB24409
ID   AAB24409 standard; protein; 241 AA.
XX
AC   AAB24409;
XX
DT   07-NOV-2000  (first entry)
XX
DE   Human PRO364 protein sequence SEQ ID NO:117.
XX
KW   Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
KW   diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
KW   angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;
KW   cytostatic; gene therapy; vaccine.
XX
OS   Homo sapiens.
XX
PN   WO200032221-A2.
XX
PD   08-JUN-2000.
XX
PF   30-NOV-1999;   99WO-US028313.
XX
PR   01-DEC-1998;   98WO-US025108.
PR   16-DEC-1998;   98US-0112850P.
PR   12-JAN-1999;   99US-0115554P.
PR   08-MAR-1999;   99WO-US005028.
PR   12-MAR-1999;   99US-0123957P.
PR   28-APR-1999;   99US-0131445P.
PR   14-MAY-1999;   99US-0134287P.
PR   02-JUN-1999;   99WO-US012252.
PR   23-JUN-1999;   99US-0141037P.
PR   20-JUL-1999;   99US-0144758P.
PR   26-JUL-1999;   99US-0145698P.
PR   01-SEP-1999;   99WO-US020111.
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PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-OCT-1999; 99US-0162506P.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;
PI Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;
PI Smith V, Watanabe CK, Williams PM, Wood WI;
XX
DR WPI; 2000-412154/35.
DR N-PSDB; AAA77604.
XX
PT Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing
PT and treating diagnosing a cardiovascular, endothelial or angiogenic
PT disorders in mammals.
XX
PS Claim 72; Fig 44; 315pp; English.
XX
CC The present invention describes nucleic acids encoding PRO polypeptides
CC useful for preventing, diagnosing and treating diagnosing a
CC cardiovascular, endothelial or angiogenic disorder in mammals by
CC modulating cell proliferation, angiogenesis and cardiovascularisation,
CC and for identifying agonists and antagonists of these processes. The
CC nucleic acids and the proteins they encode may be used in the prevention,
CC treatment and diagnosis of diseases associated with inappropriate PRO
CC expression such as cardiovascular, endothelial or angiogenic disorders in
CC mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For
CC example, the nucleic acids (NCs) and vectors containing them and the PRO
CC polypeptide may be used to treat disorders associated with decreased PRO
CC expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent
CC nucleotide and protein sequences used in the exemplification of the
CC present invention
XX
SQ Sequence 241 AA;

Query Match 100.0%; Score 1386; DB 3; Length 241;
Best Local Similarity 100.0%; Pred. No. 2.2e-101;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60

Qy         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120

Qy        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180

Qy        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240

Qy        241 V 241
              |
Db        241 V 241
```

RESULT 8
AAB47054
ID AAB47054 standard; protein; 241 AA.
XX
AC AAB47054;
XX
DT 08-MAY-2001 (first entry)
XX
DE Human PRO364.
XX
KW PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor;
KW hGITR; ligand; hGITRL; PRO175; tumour necrosis factor receptor; TNFR;
KW human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy;
KW myocardial infarction; PGF_2alpha; trauma; cancer; angiogenesis;
KW age-related macular degeneration; antibody; periodontal disease;
KW vascular-related drug targeting; atherosclerosis; hypertension;
KW inflammatory vasculitides; Reynaud's disease; aneurysm;
KW arterial restenosis; thrombophlebitis; tumor angiogenesis; lung; liver;
KW fibrosis; neuropathy; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1. .26
FT /note= "Potential signal peptide"
FT Modified-site 146
FT /note= "N-glycosylated"
FT Domain 162. .180
FT /note= "Potential transmembrane domain"
XX
PN WO200103720-A2.
XX
PD 18-JAN-2001.
XX
PF 11-JUL-2000; 2000WO-US018867.
XX
PR 12-JUL-1999; 99US-0143304P.
XX
PA (GETH) GENENTECH INC.
XX
PI Williams PM, Gerritsen ME;
XX
DR WPI; 2001-138257/14.
DR N-PSDB; AAC85433.
XX
PT Composition for diagnosing and treating cardiovascular, endothelial and
PT angiogenic disorders, comprises a PRO364 or PRO175 polypeptide.
XX
PS Claim 1; Fig 1; 76pp; English.
XX
CC This sequence represents PRO364 polypeptide, which is a human gluco-
CC corticoid-induced tumor necrosis factor receptor (hGITR). The
CC corresponding ligand (hGITRL), PRO175, is given in AAB47056. PRO364 and
CC PRO175 may be used in a mixture with a cardiovascular, endothelial,
CC angiogenic or angiostatic agent for the treatment of a cardiovascular,
CC endothelial, angiogenic or angiostatic disorder. The PRO364 cDNA sequence
CC was isolated from an expressed sequence tag (EST) database as having
CC homology to members of the tumour necrosis factor receptor (TNFR) family
CC of polypeptides. The PRO175 cDNA sequence was isolated from a library of
CC cDNA fragments derived from human umbilical vein endothelial cells
CC (HUVEC). Administering an effective amount of PRO364 or PRO175 or their
CC antagonists is useful for treating cardiac hypertrophy (which is
CC initiated by myocardial infarction and characterized by the presence of
CC an elevated level of PGF_2alpha), trauma, a cancer, or age-related
CC macular degeneration in a human. Administering a therapeutically
CC effective amount of an antibody that binds PRO364 or PRO175 is useful for
CC inhibiting angiogenesis induced by PRO364 or PRO175 in a human suffering
CC from a tumor or a retinal disorder. PRO364 or PRO175, or their
CC antagonists, are useful for vascular-related drug targeting or as
CC therapeutic targets for the treatment or prevention of atherosclerosis,
CC hypertension, inflammatory vasculitides, Reynaud's disease, aneurysms,
CC arterial restenosis, thrombophlebitis, tumor angiogenesis, gut protection
CC or regeneration and treatment of lung or liver fibrosis, periodontal
CC diseases, attraction of bone-forming cells, central and peripheral
CC nervous system disease and neuropathies and rheumatoid arthritis
XX
SQ Sequence 241 AA;

Query Match 100.0%; Score 1386; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 2.2e-101;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60

Qy         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120

Qy        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180

Qy        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240

Qy        241 V 241
              |
Db        241 V 241
```

RESULT 9
AAB20115
ID AAB20115 standard; protein; 241 AA.
XX
AC AAB20115;
XX
DT 30-APR-2001 (first entry)
XX
DE Human immunostimulant PRO364.
XX
KW PRO364; UNQ319; human; immune disease; autoimmune disease; antirheumatic;
KW antiarthritic; antiinflammatory; antianaemic; immunosuppressive;
KW antithyroid; antidiabetic; neuroprotective; hepatotropic; virucide;
KW dermatological; antipsoriatic; antiasthmatic; antiallergic;
KW immunostimulant.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	Peptide	1. .25
FT		/label= Signal_peptide
FT	Modified-site	5. .11
FT		/note= "N-myristoylation site"
FT	Modified-site	8. .14
FT		/note= "N-myristoylation site"
FT	Modified-site	25. .31
FT		/note= "N-myristoylation site"
FT	Protein	26. .241
FT		/label= Mature_protein
FT	Modified-site	30. .36
FT		/note= "N-myristoylation site"
FT	Modified-site	33. .39
FT		/note= "N-myristoylation site"
FT	Modified-site	118. .124
FT		/note= "N-myristoylation site"
FT	Modified-site	122. .128
FT		/note= "N-myristoylation site"
FT	Modified-site	146. .150
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	156. .162
FT		/note= "N-myristoylation site"
FT	Domain	163. .183
FT		/note= "transmembrane domain"
FT	Peptide	166. .177
FT		/note= "prokaryotic membrane lipoprotein lipid attachment site"
FT	Peptide	171. .193
FT		/note= "leucine zipper pattern"

XX
PN WO200105972-A1.
XX
PD 25-JAN-2001.
XX
PF 15-MAR-2000; 2000WO-US006884.
XX
PR 20-JUL-1999; 99US-0144758P.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ;
PI Gurney AL, Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D;
PI Watanabe CK, Wood WI;
XX
DR WPI; 2001-103149/11.
DR N-PSDB; AAF30057.
XX
PT New PRO polypeptides, nucleic acids and (ant)agonists, useful for
PT diagnosing and treating immune-related disorders, such as multiple
PT sclerosis, rheumatoid arthritis and diabetes.
XX
PS Claim 20; Fig 16; 127pp; English.
XX
CC The present sequence is that of novel human immunomodulator PRO364
CC (UNQ319), as deduced from cDNA (see AAF30057) isolated from a small
CC intestine library. PRO364 (26 kDa, pI 6.34) shows sequence homology to
CC mouse GITR protein and may be its human counterpart. The invention
CC provides polynucleotides (see AAF30050-62) encoding novel human PRO
CC proteins (see AAB20108-20) including PRO364. Claimed compositions
CC comprising these proteins or their agonists are useful for increasing
CC infiltration of inflammatory cells into a tissue of a mammal, stimulating
CC or enhancing an immune response, or increasing the proliferation of T-
CC lymphocytes in a mammal in response to an antigen. Claimed compositions
CC comprising a PRO polypeptide or its antagonist have the opposite effect.
CC A claimed method for treating an immune related disorder, such as a T
CC cell disorder, involves administering a PRO polypeptide, an agonist
CC antibody or an antagonist antibody. The disorder is selected from
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, spondyloarthropathy, systemic sclerosis,
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, demyelinated diseases (such as multiple sclerosis), autoimmune
CC chronic active hepatitis, primary biliary cirrhosis, granulomatous
CC hepatitis, sclerosing cholangitis, inflammatory bowel disease (ulcerative
CC colitis and Crohn's disease), gluten-sensitive enteropathy, Whipple's
CC disease, (auto)immune-mediated skin diseases (such as bullous skin
CC disease, erythema multiforme and psoriasis), allergic diseases (such as
CC asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and
CC urticaria), immunologic diseases of the lung and transplantation
CC associated diseases (such as graft rejection and graft-versus-host
CC disease) (all claimed). Claimed methods of diagnosing these disorders
CC comprise detecting the level of expression of the PRO gene. Also claimed
CC are a method of identifying a compound capable of inhibiting the
CC expression or activity of the PRO polypeptide, vectors, host cells,
CC antibodies, and a method of stimulating the proliferation of T
CC lymphocytes using PRO364
XX
SQ Sequence 241 AA;

Query Match 100.0%; Score 1386; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 2.2e-101;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60

Qy         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120

Qy        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
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Qy        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240

Qy        241 V 241
              |
Db        241 V 241
```

RESULT 10
AAB53090
ID AAB53090 standard; protein; 241 AA.
XX
AC AAB53090;
XX
DT 28-FEB-2001 (first entry)
XX
DE Human angiogenesis-associated protein PRO364, SEQ ID NO:142.
XX
KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;
KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
KW Alzheimer's disease; Huntington's disease; stroke; drug screening;
KW gene therapy; transgenic animal.
XX
OS Homo sapiens.
XX
PN WO200053753-A2.
XX
PD 14-SEP-2000.
XX
PF 05-JAN-2000; 2000WO-US000219.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 14-MAY-1999; 99US-0134287P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;
PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;
XX
DR WPI; 2001-090793/10.
DR N-PSDB; AAC97479.
XX
PT New isolated nucleic acid for producing a PRO polypeptide, analyzing
PT genetic disorders and treating cardiovascular, endothelial or angiogenic
PT disorders, such as atherosclerosis, wounds or cancer.
XX
PS Claim 69; Fig 54; 293pp; English.
XX
CC The invention relates to novel human angiogenesis-associated proteins
CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding
CC PRO proteins. The invention also relates to vectors and host cells
CC comprising a PRO nucleic acid, the recombinant production of a PRO
CC protein, PRO antibodies specific for a PRO protein, fusion proteins
CC comprising a PRO protein, agonists or antagonists of a PRO protein, and
CC compounds which inhibit the expression of a PRO gene. The invention
CC additionally encompasses methods of identifying modulators of PRO
CC expression or activity; diagnosing a cardiovascular, endothelial or
CC angiogenic disorder, or a susceptibility to such a disorder by detecting
CC mutations in a PRO gene, or the expression level of a PRO gene within a
CC particular tissue; treating a cardiovascular, endothelial or angiogenic
CC disorder via the administration of a PRO protein, PRO nucleic acid, or
CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a
CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial
CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the
CC administration of a PRO protein, or an agonist or antagonist thereof. PRO
CC nucleic acids, PRO proteins, antibodies against PRO proteins, PRO
CC agonists and PRO antagonists may be used as therapeutic agents to treat
CC cardiovascular, endothelial or angiogenic disorders, such as
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,
CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's
CC disease, or stroke. PRO nucleic acids are additionally useful in the
CC recombinant production of PRO proteins, as hybridisation probes to screen
CC libraries to isolate cDNAs with sequence identity to PRO proteins, to map
CC genes encoding PRO proteins, to analyse genetic disorders, and in gene
CC therapy. PRO nucleic acids can also be used to produce transgenic animals
CC useful for the development and screening of potential therapeutic agents.
CC The present sequence represents a PRO protein of the invention
XX
SQ Sequence 241 AA;

Query Match 100.0%; Score 1386; DB 4; Length 241;
Best Local Similarity 100.0%; Pred. No. 2.2e-101;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60

Qy         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120

Qy        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180

Qy        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240

Qy        241 V 241
              |
Db        241 V 241
```

RESULT 11
AAB47289
ID AAB47289 standard; protein; 241 AA.
XX
AC AAB47289;
XX
DT 22-AUG-2001 (first entry)
XX
DE PRO364 polypeptide.
XX
KW PRO; type II transmembrane protein; tumour necrosis factor; stroke;
KW heart hypertrophy; cardiovascular; endothelial; angiogenic; disorder;
KW myocardial infarction; cardiac hypertrophy; PGF_2alpha; trauma; bone;
KW cancer; age-related macular degeneration; wound; burn; hypertension;
KW diabetes mellitus; osteoporosis; ischaemia; atherosclerosis; psoriasis;
KW rheumatoid arthritis; Crohn's disease; amylotrophic lateral sclerosis;
KW endometriosis; angina; neoplasms; periodontal disease; cartilage; TNF;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease.
XX
OS Homo sapiens.
XX

```
FH   Key             Location/Qualifiers
FT   Peptide         1. .25
FT                   /label= Signal peptide
FT   Modified-site   5. .11
FT                   /label= N-myristoylation site
FT   Modified-site   8. .14
FT                   /label= N-myristoylation site
FT   Modified-site   25. .31
FT                   /label= N-myristoylation site
FT   Protein         26. .241
FT                   /label= Mature PRO364
FT   Modified-site   30. .36
FT                   /label= N-myristoylation site
FT   Modified-site   33. .39
FT                   /label= N-myristoylation site
FT   Modified-site   118. .124
FT                   /label= N-myristoylation site
FT   Modified-site   122. .128
FT                   /label= N-myristoylation site
FT   Modified-site   146. .150
FT                   /label= N-linked glycosylation site
FT   Modified-site   156. .162
FT                   /label= N-myristoylation site
FT   Domain          162. .180
FT                   /label= Potential transmembrane domain
FT   Binding-site    166. .177
FT                   /label= Prokaryotic membrane lipoprotein attachment site
FT   Domain          171. .193
FT                   /label= Leucine zipper
XX
PN   WO200140464-A1.
XX
PD   07-JUN-2001.
XX
PF   11-AUG-2000; 2000WO-US022031.
XX
PR   30-NOV-1999;   99WO-US028313.
PR   30-NOV-1999;   99WO-US028409.
PR   05-JAN-2000; 2000WO-US000219.
PR   24-FEB-2000; 2000WO-US005004.
PR   15-MAR-2000; 2000WO-US006884.
PR   30-MAR-2000; 2000WO-US008439.
PR   17-MAY-2000; 2000WO-US013705.
PR   30-MAY-2000; 2000WO-US014941.
PR   28-JUL-2000; 2000WO-US020710.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Ferrara N,  Godowski PJ,  Gurney AL;
PI   Hillan KJ,  Mark MR,  Marsters SA,  Paoni NF,  Pitti RM,  Wood WI;
XX
DR   WPI; 2001-381383/40.
DR   N-PSDB; AAC85947.
XX
PT   Isolated PRO polypeptide useful in treating and diagnosing a
PT   cardiovascular, endothelial or angiogenic disorder e.g. cancer, diabetes
PT   mellitus, myocardial infarction, arthritis.
XX
PS   Claim 56; Fig 6; 144pp; English.
XX
CC   The sequences given in AAB47287-90 show PRO polypeptides. PRO175 shows
CC   type II transmembrane protein typology, and portions of PRO364 show
CC   homology to members of the tumour necrosis factor (TNF) family, thereby
CC   indicating that it may be a novel member of the TNF family. PRO175 and
CC   PRO185 stimulated heart hypertrophy. PRO cDNA's may be used to identify a
CC   compound that inhibits PRO, diagnosing a cardio- vascular, endothelial or
CC   angiogenic disorder in a mammal by detecting PRO cDNA, treating
CC   cardiovascular, endothelial or angiogenic disorder in a mammal, and
CC   inducing cardiac hypertrophy or inhibiting endothelial cell growth or
CC   angiogenesis in a mammal. The mammal is a human which has suffered
CC   myocardial infarction, cardiac hypertrophy characterized by the presence
CC   of elevated PGF_2alpha, trauma, cancer or age-related macular
CC   degeneration. Trauma includes wounds or burns. Other treatable diseases
CC   include diabetes mellitus, osteoporosis, ischaemia, hypertension,
CC   rheumatoid arthritis, Crohn's disease, atherosclerosis, psoriasis,
CC   endometriosis, angina, neoplasms, periodontal disease, bone and cartilage
CC   repair, Alzheimer's disease, Parkinson's disease, Huntington's disease,
CC   amylotrophic lateral sclerosis, and stroke
XX
SQ   Sequence 241 AA;

  Query Match             100.0%;  Score 1386;  DB 4;  Length 241;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-101;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60

Qy         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120

Qy        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180

Qy        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240

Qy        241 V 241
              |
Db        241 V 241


RESULT 12
AAB50982
ID   AAB50982 standard; protein; 241 AA.
XX
AC   AAB50982;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human PRO364 protein.
XX
KW   Human; PRO; cardiant; antiangiogenic; antiarteriosclerotic; hypotensive;
KW   vasotropic; antirheumatic; antiarthritic; antiinflammatory; cytostatic;
KW   vulnerary; antianginal; gene therapy; cardiovascular disease;
KW   endothelial disorder; angiogenic disorder; cancer; periodontal disease;
KW   wound healing.
XX
OS   Homo sapiens.
XX
PN   WO200073445-A2.
XX
PD   07-DEC-2000.
XX
PF   17-MAY-2000; 2000WO-US013705.
XX
PR   02-JUN-1999;   99WO-US012252.
PR   23-JUN-1999;   99US-0141037P.
PR   20-JUL-1999;   99US-0144758P.
PR   26-JUL-1999;   99US-0145698P.
PR   28-JUL-1999;   99US-0146222P.
PR   01-SEP-1999;   99WO-US020111.
PR   30-NOV-1999;   99WO-US028313.
PR   30-NOV-1999;   99WO-US028409.
PR   02-DEC-1999;   99WO-US028565.
PR   16-DEC-1999;   99WO-US030095.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   24-FEB-2000; 2000WO-US005004.
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PR   02-MAR-2000; 2000WO-US005841.
PR   10-MAR-2000; 2000WO-US006319.
PR   15-MAR-2000; 2000WO-US006884.
PR   21-MAR-2000; 2000WO-US007532.
PR   30-MAR-2000; 2000WO-US008439.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Ferrara N,  Gerber H,  Gerritsen ME;
PI   Goddard A,  Godowski PJ,  Gurney AL,  Kuo SS,  Mark MR,  Marsters SA;
PI   Paoni NF,  Pitti RM,  Watanabe CK,  Williams PM,  Wood WI;
XX
DR   WPI; 2001-025251/03.
DR   N-PSDB; AAC90566.
XX
PT   Seventeen nucleic acids encoding PRO polypeptides which are useful in
PT   diagnosis and treatment of cardiovascular, endothelial or angiogenic
PT   disorders in a mammal.
XX
PS   Claim 71; Fig 8; 182pp; English.
XX
CC   The present sequence is one of seventeen novel PRO polypeptides. The PRO
CC   nucleic acids, polypeptides, agonists and antagonists are useful for
CC   treating cardiovascular, endothelial or angiogenic disorders in a mammal.
CC   Examples of these disorders include cardiac hypertrophy, trauma, cancer,
CC   age-related macular degeneration, atherosclerosis, hypertension, arterial
CC   restenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial
CC   infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and
CC   antagonists are also used to prevent tumour angiogenesis and for treating
CC   periodontal diseases. They are also used to stimulate wound healing and
CC   tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO
CC   antibodies are useful for diagnosing a cardiovascular, endothelial or
CC   angiogenic disorder
XX
SQ   Sequence 241 AA;

  Query Match             100.0%;  Score 1386;  DB 4;  Length 241;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-101;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60

Qy         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120

Qy        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180

Qy        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240

Qy        241 V 241
              |
Db        241 V 241


RESULT 13
AAB50910
ID   AAB50910 standard; protein; 241 AA.
XX
AC   AAB50910;
XX
DT   21-MAR-2001  (first entry)
XX
DE   Human PRO364 protein.
XX
KW   Human; PRO; antiinflammatory; dermatological; antiarthritic;
KW   antirheumatic; cardiant; antianaemic; immunosuppressive; antithyroid;
KW   antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;
KW   antiallergic; antiasthmatic; immune related disorder;
KW   hepatobiliary disease; autoimmune disease; allergy.
XX
OS   Homo sapiens.
XX
PN   WO200073452-A2.
XX
PD   07-DEC-2000.
XX
PF   02-JUN-2000; 2000WO-US015264.
XX
PR   02-JUN-1999;   99WO-US012252.
PR   20-JUL-1999;   99US-0144732P.
PR   20-JUL-1999;   99US-0144758P.
PR   28-JUL-1999;   99US-0146222P.
PR   01-SEP-1999;   99WO-US020111.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   29-OCT-1999;   99US-0162506P.
PR   30-NOV-1999;   99WO-US028313.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028565.
PR   09-DEC-1999;   99US-0170262P.
PR   20-DEC-1999;   99WO-US030911.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   24-FEB-2000; 2000WO-US004914.
PR   24-FEB-2000; 2000WO-US005004.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   03-MAR-2000; 2000US-0187202P.
PR   15-MAR-2000; 2000WO-US006884.
PR   20-MAR-2000; 2000WO-US007377.
PR   21-MAR-2000; 2000WO-US007532.
PR   30-MAR-2000; 2000WO-US008439.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Chan B,  Goddard A,  Godowski PJ;
PI   Gurney AL,  Hebert C,  Henzel W,  Kabakoff RC,  Shelton DL,  Tumas D;
PI   Watanabe CK,  Wood WI;
XX
DR   WPI; 2001-025253/03.
DR   N-PSDB; AAC91469.
XX
PT   Thirty three nucleic acids encoding PRO polypeptides which are useful in
PT   the diagnosis and treatment of immune related disorders, e.g. systemic
PT   lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis
PT   and diabetes mellitus.
XX
PS   Claim 58; Fig 18; 218pp; English.
XX
CC   The present sequence is one of thirty three novel PRO polypeptides. The
CC   PRO polypeptides, anti-PRO antibodies, agonists and antagonists are
CC   useful for treating and diagnosing immune related disorders such as
CC   systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC   juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis,
CC   idiopathic inflammatory myopathies, Sjogren's syndrome, systemic
CC   vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC   thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC   disease, demyelinating diseases of the central and peripheral nervous
CC   systems (such as multiple sclerosis, idiopathic demyelinating
CC   polyneuropathy or Guillain-Barre syndrome, and chronic inflammatory
CC   demyelinating polyneuropathy), hepatobiliary diseases (such as
CC   infectious, autoimmune chronic active hepatitis, primary biliary
```

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CC   cirrhosis, granulomatous hepatitis and sclerosing cholangitis),
CC   inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's
CC   disease, autoimmune or immune-mediated skin diseases (such as bullous
CC   skin diseases, erythema multiforme, contact dermatitis, psoriasis),
CC   allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,
CC   food hypersensitivity and urticaria), immunological diseases of the lung
CC   (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis and
CC   hypersensitivity pneumonitis), transplantation associated diseases
CC   including graft rejection and graft-versus-host diseases
XX
SQ   Sequence 241 AA;

  Query Match             100.0%;  Score 1386;  DB 4;  Length 241;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-101;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60

Qy         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120

Qy        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180

Qy        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240

Qy        241 V 241
              |
Db        241 V 241


RESULT 14
AAE28161
ID   AAE28161 standard; protein; 241 AA.
XX
AC   AAE28161;
XX
DT   27-DEC-2002  (first entry)
XX
DE   Human TR11 receptor protein #2.
XX
KW   Human; tumour necrosis factor receptor; TNF; allergic encephalomyelitis;
KW   autoimmune disease; autoimmune haemolytic anaemia; multiple sclerosis;
KW   systemic lupus erythematosus; Goodpasture's syndrome; diabetes mellitus;
KW   rheumatoid arthritis; Sjogren's syndrome; scleroderma; immunodeficiency;
KW   urticaria; DiGeorge anomaly; natural killer deficiency; asthma; allergy;
KW   inflammatory condition; respiratory disorder; graft-versus-host-disease;
KW   transplantation rejection; type II collagen-induced arthritis; cancer;
KW   cardiovascular disorder; atherosclerosis; gastrointestinal disorder;
KW   myocarditis; inflammatory bowel disease; traumatic brain injury; stroke;
KW   Alzheimer's disease; inflammation; trauma; septic shock; thrombolytic;
KW   gout; haemostatic; blood coagulation disorder; blood platelet disorder;
KW   thrombocytopaenia; wound; trauma; surgery; gene therapy; immuno therapy;
KW   TR11 receptor.
XX
OS   Homo sapiens.
XX
PN   US2002098525-A1.
XX
PD   25-JUL-2002.
XX
PF   27-JUL-2001; 2001US-00915593.
XX
PR   21-OCT-1997;   97US-0063212P.
PR   21-OCT-1998;   98US-00176200.
PR   24-FEB-1999;   99US-0121648P.
PR   13-MAY-1999;   99US-0134172P.
PR   16-JUL-1999;   99US-0144076P.
PR   23-FEB-2000; 2000US-00512363.
PR   28-JUL-2000; 2000US-0221577P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ni J,  Ruben SM;
XX
DR   WPI; 2002-673824/72.
XX
PT   Novel antibody or its portion which specifically binds to two tumor
PT   necrosis factor receptor-related protein splice variants, TR11SV1 and
PT   TR11SV2, useful for treating autoimmune hemolytic anemia, and
PT   Goodpasture's syndrome.
XX
PS   Disclosure; Page 122; 135pp; English.
XX
CC   The present invention relates to novel antibodies or their portion which
CC   specifically bind tumour necrosis factor (TNF) receptor-related protein
CC   splice variants, TR11SV1 or TR11SV2. Sequences of the invention are
CC   useful for treating, detecting and/or preventing diseases, disorders or
CC   conditions associated with aberrant expression and/or activity of TR11,
CC   TR11SV1 and TR11SV2 polypeptides, e.g., autoimmune diseases such as
CC   autoimmune haemolytic anaemia, allergic encephalomyelitis, multiple
CC   sclerosis, systemic lupus erythematosus, Goodpasture's syndrome, diabetes
CC   mellitus, rheumatoid arthritis, Sjogren's syndrome, scleroderma with anti
CC   -collagen antibodies, urticaria, conditions associated with immuno-
CC   deficiency e.g. T-cell related deficiencies such as DiGeorge anomaly,
CC   natural killer deficiency, inflammatory conditions such as respiratory
CC   disorders (e.g. asthma, allergy), allergic reactions such as asthma,
CC   graft-versus-host-disease, transplantation rejections, type II collagen-
CC   induced arthritis, cancers (ovarian lung, bladder or liver cancer),
CC   cardiovascular disorders (atherosclerosis, myocarditis), gastrointestinal
CC   disorders (inflammatory bowel disease), central nervous system disorders
CC   (e.g. traumatic brain injury, Alzheimer's disease, stroke) and disorders
CC   characterised by inflammation (e.g. gout, trauma, septic shock). They are
CC   used for modulating haemostatic or thrombolytic activity and thus is used
CC   for treating blood coagulation disorders, the blood platelet disorders
CC   (e.g. thrombocytopaenia) or wounds resulting from trauma, surgery or
CC   other causes. Polynucleotides of the invention are useful in gene therapy
CC   and immuno therapy. The present sequence is human TR11 receptor protein
XX
SQ   Sequence 241 AA;

  Query Match             100.0%;  Score 1386;  DB 5;  Length 241;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-101;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60

Qy         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120

Qy        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180

Qy        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240

Qy        241 V 241
              |
Db        241 V 241


RESULT 15
ABU08442
ID   ABU08442 standard; protein; 241 AA.
XX
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```
AC   ABU08442;
XX
DT   13-JUN-2003  (first entry)
XX
DE   Amino acid sequence for human TR11 polypeptide.
XX
KW   Human; tumour necrosis factor receptor family; TNF receptor; TR11;
KW   endokine-alpha; endokine-alpha receptor; immunodeficiency disease;
KW   severe combined immunodeficiency-X linked; SCID-X linked; SLE;
KW   Bruton's disease; dysgammaglobulinaemia; autoimmune disease;
KW   systemic lupus erythematosus; rheumatoid arthritis; dermatitis;
KW   allergic encephalomyelitis; immunostimulant; dermatological;
KW   immunosuppressive; antiinflammatory; antirheumatic; antiarthritic;
KW   antiallergic.
XX
OS   Homo sapiens.
XX
PN   US6503184-B1.
XX
PD   07-JAN-2003.
XX
PF   23-FEB-2000; 2000US-00512363.
XX
PR   21-OCT-1997;   97US-0063212P.
PR   21-OCT-1998;   98US-00176200.
PR   24-FEB-1999;   99US-0121648P.
PR   13-MAY-1999;   99US-0134172P.
PR   16-JUL-1999;   99US-0144076P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ni J,  Ruben SM;
XX
DR   WPI; 2003-352213/33.
XX
PT   Inhibiting binding of endokine-alpha to endogenous endokine-alpha
PT   receptors in a mammal, by administering to a mammal a fragment of human
PT   tumor necrosis factor receptor-related protein.
XX
PS   Disclosure; Col 201-202; 114pp; English.
XX
CC   The present invention relates to the isolation of novel members of the
CC   tumour necrosis factor (TNF) family of receptors, referred to as TNF
CC   receptor-related proteins and designated TR11, TR11SV1 and TR11SV2.
CC   TR11SV1 and TR11SV2 represent splice variants of TR11. The invention also
CC   discloses the polynucleotide sequences encoding the TR11 receptors, and a
CC   method of inhibiting endokine-alpha binding to endogenous endokine-alpha
CC   receptors in mammals. The method of the invention is useful for
CC   inhibiting the binding of endokine-alpha to endogenous endokine-alpha
CC   receptors in a mammal, preferably humans. The method is useful for
CC   treating or preventing immunodeficiency diseases (e.g. severe combined
CC   immunodeficiency (SCID)-X linked, Bruton's disease,
CC   dysgammaglobulinaemia), and autoimmune diseases (e.g. systemic lupus
CC   erythematosus (SLE), rheumatoid arthritis, dermatitis, allergic
CC   encephalomyelitis). The present sequence represents human TR11
CC   polypeptide
XX
SQ   Sequence 241 AA;

  Query Match             100.0%;  Score 1386;  DB 6;  Length 241;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-101;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        241 V 241
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Db        241 V 241


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Job time : 142.311 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 26, 2005, 15:51:55 ; Search time 115.618 Seconds
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Gapop 10.0 , Gapext 0.5

Searched: 1862994 seqs, 417510619 residues

Total number of hits satisfying chosen parameters: 1862994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1386	100.0	241	9	US-09-915-593-28	Sequence 28, Appl
2	1386	100.0	241	13	US-10-116-378-3	Sequence 3, Appli
3	1386	100.0	241	14	US-10-283-105-28	Sequence 28, Appl
4	1386	100.0	241	14	US-10-277-966-28	Sequence 28, Appl
5	1386	100.0	241	15	US-10-295-027-1284	Sequence 1284, Ap
6	1386	100.0	241	17	US-10-959-537-3	Sequence 3, Appli
7	1386	100.0	241	20	US-11-032-294-3	Sequence 3, Appli
8	1382	99.7	240	16	US-10-783-528-75	Sequence 75, Appl
9	1322.5	95.4	234	9	US-09-915-593-2	Sequence 2, Appli
10	1322.5	95.4	234	14	US-10-283-105-2	Sequence 2, Appli
11	1322.5	95.4	234	14	US-10-277-966-2	Sequence 2, Appli
12	1306.5	94.3	246	15	US-10-264-237-1762	Sequence 1762, Ap
13	1274.5	92.0	240	9	US-09-915-593-6	Sequence 6, Appli
14	1274.5	92.0	240	14	US-10-283-105-6	Sequence 6, Appli
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16	1056	76.2	241	9	US-09-915-593-4	Sequence 4, Appli
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19	953	68.8	317	13	US-10-116-378-26	Sequence 26, Appl
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21	735.5	53.1	228	9	US-09-915-593-7	Sequence 7, Appli
22	735.5	53.1	228	13	US-10-116-378-24	Sequence 24, Appl
23	735.5	53.1	228	14	US-10-283-105-7	Sequence 7, Appli
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25	735.5	53.1	228	17	US-10-959-537-24	Sequence 24, Appl
26	255	18.4	89	10	US-09-866-050A-191	Sequence 191, App
27	201.5	14.5	276	15	US-10-369-300-4	Sequence 4, Appli
28	197	14.2	256	13	US-10-027-199-10	Sequence 10, Appl
29	197	14.2	256	14	US-10-067-122-2	Sequence 2, Appli
30	197	14.2	256	17	US-10-981-352-4	Sequence 4, Appli
31	195.5	14.1	255	9	US-09-739-394-9	Sequence 9, Appli
32	195.5	14.1	255	9	US-09-826-212-11	Sequence 11, Appl
33	195.5	14.1	255	9	US-09-935-727-13	Sequence 13, Appl
34	195.5	14.1	255	10	US-09-877-336-2	Sequence 2, Appli
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40	195.5	14.1	255	14	US-10-207-655-160	Sequence 160, App
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42	195.5	14.1	255	16	US-10-646-308-18	Sequence 18, Appl
43	195.5	14.1	255	16	US-10-755-889-174	Sequence 174, App
44	195.5	14.1	255	16	US-10-748-112-15	Sequence 15, Appl
45	195.5	14.1	255	16	US-10-723-860-588	Sequence 588, App

ALIGNMENTS

RESULT 1
US-09-915-593-28
; Sequence 28, Application US/09915593
; Patent No. US20020098525A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
; TITLE OF INVENTION: TR11, TR11SV1, and TR11SV2
; FILE REFERENCE: PF396P2
; CURRENT APPLICATION NUMBER: US/09/915,593
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/221,577
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 09/512,363
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/144,076
; PRIOR FILING DATE: 2000-07-16
; PRIOR APPLICATION NUMBER: 60/134,172
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/121,648
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 09/176,200
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/063,212
; PRIOR FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-593-28

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  Best Local Similarity  100.0%;  Pred. No. 1.1e-106;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
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Qy        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
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Qy        241 V 241
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Db        241 V 241


RESULT 2
US-10-116-378-3
; Sequence 3, Application US/10116378
; Publication No. US20020150993A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi J.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Gurney, Austin
;  APPLICANT:  Marsters, Scot A.
;  APPLICANT:  Pitti, Robert M.
;  APPLICANT:  Wood, William
;  TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND
;  TITLE OF INVENTION:  NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P1206R1
;  CURRENT APPLICATION NUMBER: US/10/116,378
;  CURRENT FILING DATE:  2002-04-04
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
;  NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 3
;   LENGTH: 241
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-116-378-3

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  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
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Qy        241 V 241
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Db        241 V 241


RESULT 3
US-10-283-105-28
; Sequence 28, Application US/10283105
; Publication No. US20030138426A1
; GENERAL INFORMATION:
;  APPLICANT: Ni, Jian
;  APPLICANT:  Ruben, Steven M
;  TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,
;  TITLE OF INVENTION:  TR11Sv22
;  FILE REFERENCE: PF396P3
;  CURRENT APPLICATION NUMBER: US/10/283,105
;  CURRENT FILING DATE:  2002-10-30
;  PRIOR APPLICATION NUMBER: 60/330,757
;  PRIOR FILING DATE: 2001-10-30
;  PRIOR APPLICATION NUMBER: 09/915,593
;  PRIOR FILING DATE: 2001-07-27
;  PRIOR APPLICATION NUMBER: 60/221,577
;  PRIOR FILING DATE: 2000-07-28
;  PRIOR APPLICATION NUMBER: 09/512,363
;  PRIOR FILING DATE: 2000-02-23
;  PRIOR APPLICATION NUMBER: 60/144,076
;  PRIOR FILING DATE: 1999-07-16
;  PRIOR APPLICATION NUMBER: 60/134,172
;  PRIOR FILING DATE: 1999-05-13
;  PRIOR APPLICATION NUMBER: 60/121,648
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 09/176,200
;  PRIOR FILING DATE: 1998-10-21
;  PRIOR APPLICATION NUMBER: 60/063,212
;  PRIOR FILING DATE: 1997-10-21
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
;   LENGTH: 241
;   TYPE: PRT
;   ORGANISM: human
US-10-283-105-28

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Db        241 V 241


RESULT 4
US-10-277-966-28
; Sequence 28, Application US/10277966
; Publication No. US20030153499A1
; GENERAL INFORMATION:
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; APPLICANT: Ni, Jian
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,
; TITLE OF INVENTION: TR11SV2
; FILE REFERENCE: PF396P1D1
; CURRENT APPLICATION NUMBER: US/10/277,966
; CURRENT FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 09/512,363
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/121,648
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/134,172
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/144,076
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/176,200
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/063,212
; PRIOR FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 241
; TYPE: PRT
; ORGANISM: human
US-10-277-966-28

Query Match 100.0%; Score 1386; DB 14; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.1e-106;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
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Qy         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
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Qy        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
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Qy        241 V 241
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Db        241 V 241
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RESULT 5
US-10-295-027-1284
; Sequence 1284, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynne, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1284
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-1284

Query Match 100.0%; Score 1386; DB 15; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.1e-106;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
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Qy        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240

Qy        241 V 241
              |
Db        241 V 241
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RESULT 6
US-10-959-537-3
; Sequence 3, Application US/10959537
; Publication No. US20050069983A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pitti, Robert M.
; APPLICANT: Wood, William
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P1206R1
; CURRENT APPLICATION NUMBER: US/10/959,537
; CURRENT FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US/09/247,225
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: US 60/074,087
; PRIOR FILING DATE: 1998-02-09

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;  NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 3
;   LENGTH: 241
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-959-537-3

  Query Match             100.0%;  Score 1386;  DB 17;  Length 241;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-106;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60

Qy         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120

Qy        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180

Qy        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240

Qy        241 V 241
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Db        241 V 241


RESULT 7
US-11-032-294-3
; Sequence 3, Application US/11032294
; Publication No. US20050202008A1
; GENERAL INFORMATION:
;  APPLICANT: P. Mickey Williams
;  APPLICANT:  Mary E. Gerritsen
;  TITLE OF INVENTION: PROMOTION OR INHIBITION OF ANGIOGENESIS AND
;  TITLE OF INVENTION:  CARDIOVASCULARIZATION BY TUMOR NECROSIS FACTOR
;  TITLE OF INVENTION:  LIGAND/RECEPTOR HOMOLOGS
;  FILE REFERENCE: P1765R1
;  CURRENT APPLICATION NUMBER: US/11/032,294
;  CURRENT FILING DATE:  2005-01-10
;  PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/613,972
;  PRIOR FILING DATE: CURRENT FILING DATE:  2000-07-11
;  PRIOR APPLICATION NUMBER: US 60/143,304
;  PRIOR FILING DATE: 1999-07-12
;  NUMBER OF SEQ ID NOS: 22
; SEQ ID NO 3
;   LENGTH: 241
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-032-294-3

  Query Match             100.0%;  Score 1386;  DB 20;  Length 241;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-106;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60

Qy         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120

Qy        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180

Qy        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240

Qy        241 V 241
              |
Db        241 V 241


RESULT 8
US-10-783-528-75
; Sequence 75, Application US/10783528
; Publication No. US20040219579A1
; GENERAL INFORMATION:
;  APPLICANT: Aziz, Natasha
;  APPLICANT:  Gish, Kurt
;  APPLICANT:  Wilson, Keith
;  APPLICANT:  Zlotnik, Albert
;  TITLE OF INVENTION: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND
;  FILE REFERENCE: 05882.0191.NPUS01
;  CURRENT APPLICATION NUMBER: US/10/783,528
;  CURRENT FILING DATE:  2004-02-19
;  NUMBER OF SEQ ID NOS: 116
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 75
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-783-528-75

  Query Match             99.7%;  Score 1382;  DB 16;  Length 240;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-106;
  Matches  240;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60

Qy         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120

Qy        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180

Qy        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240


RESULT 9
US-09-915-593-2
; Sequence 2, Application US/09915593
; Patent No. US20020098525A1
; GENERAL INFORMATION:
;  APPLICANT: Ni, Jian
;  APPLICANT:  Ruben, Steven M.
;  TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
;  TITLE OF INVENTION:  TR11, TR11SV1, and TR11SV2
;  FILE REFERENCE: PF396P2
;  CURRENT APPLICATION NUMBER: US/09/915,593
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/221,577
;  PRIOR FILING DATE: 2000-07-28
;  PRIOR APPLICATION NUMBER: 09/512,363
;  PRIOR FILING DATE: 2000-02-23
;  PRIOR APPLICATION NUMBER: 60/144,076
;  PRIOR FILING DATE: 2000-07-16
;  PRIOR APPLICATION NUMBER: 60/134,172
;  PRIOR FILING DATE: 1999-05-13
;  PRIOR APPLICATION NUMBER: 60/121,648
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 09/176,200
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;  PRIOR FILING DATE: 1998-10-21
;  PRIOR APPLICATION NUMBER: 60/063,212
;  PRIOR FILING DATE: 1997-10-21
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;    LENGTH: 234
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-915-593-2

  Query Match             95.4%;  Score 1322.5;  DB 9;  Length 234;
  Best Local Similarity   96.7%;  Pred. No. 1.9e-101;
  Matches  233;  Conservative    1;  Mismatches    0;  Indels    7;  Gaps    1;

Qy          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60

Qy         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120

Qy        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180

Qy        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
              ||||||||||||       |:|||||||||||||||||||||||||||||||||||||||
Db        181 TSAQLGLHIWQL-------RKTQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 233

Qy        241 V 241
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Db        234 V 234


RESULT 10
US-10-283-105-2
; Sequence 2, Application US/10283105
; Publication No. US20030138426A1
; GENERAL INFORMATION:
;  APPLICANT: Ni, Jian
;  APPLICANT:  Ruben, Steven M
;  TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,
;  TITLE OF INVENTION:  TR11Sv22
;  FILE REFERENCE: PF396P3
;  CURRENT APPLICATION NUMBER: US/10/283,105
;  CURRENT FILING DATE:  2002-10-30
;  PRIOR APPLICATION NUMBER: 60/330,757
;  PRIOR FILING DATE: 2001-10-30
;  PRIOR APPLICATION NUMBER: 09/915,593
;  PRIOR FILING DATE: 2001-07-27
;  PRIOR APPLICATION NUMBER: 60/221,577
;  PRIOR FILING DATE: 2000-07-28
;  PRIOR APPLICATION NUMBER: 09/512,363
;  PRIOR FILING DATE: 2000-02-23
;  PRIOR APPLICATION NUMBER: 60/144,076
;  PRIOR FILING DATE: 1999-07-16
;  PRIOR APPLICATION NUMBER: 60/134,172
;  PRIOR FILING DATE: 1999-05-13
;  PRIOR APPLICATION NUMBER: 60/121,648
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 09/176,200
;  PRIOR FILING DATE: 1998-10-21
;  PRIOR APPLICATION NUMBER: 60/063,212
;  PRIOR FILING DATE: 1997-10-21
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;    LENGTH: 234
;    TYPE: PRT
;    ORGANISM: human
US-10-283-105-2

  Query Match             95.4%;  Score 1322.5;  DB 14;  Length 234;
  Best Local Similarity   96.7%;  Pred. No. 1.9e-101;
  Matches  233;  Conservative    1;  Mismatches    0;  Indels    7;  Gaps    1;

Qy          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60

Qy         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120

Qy        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180

Qy        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
              ||||||||||||       |:|||||||||||||||||||||||||||||||||||||||
Db        181 TSAQLGLHIWQL-------RKTQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 233

Qy        241 V 241
              |
Db        234 V 234


RESULT 11
US-10-277-966-2
; Sequence 2, Application US/10277966
; Publication No. US20030153499A1
; GENERAL INFORMATION:
;  APPLICANT: Ni, Jian
;  APPLICANT:  Ruben, Steven
;  TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,
;  TITLE OF INVENTION:  TR11SV2
;  FILE REFERENCE: PF396P1D1
;  CURRENT APPLICATION NUMBER: US/10/277,966
;  CURRENT FILING DATE:  2002-10-23
;  PRIOR APPLICATION NUMBER: 09/512,363
;  PRIOR FILING DATE: 2000-02-23
;  PRIOR APPLICATION NUMBER: 60/121,648
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 60/134,172
;  PRIOR FILING DATE: 1999-05-13
;  PRIOR APPLICATION NUMBER: 60/144,076
;  PRIOR FILING DATE: 1999-07-16
;  PRIOR APPLICATION NUMBER: 09/176,200
;  PRIOR FILING DATE: 1998-10-21
;  PRIOR APPLICATION NUMBER: 60/063,212
;  PRIOR FILING DATE: 1997-10-21
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;    LENGTH: 234
;    TYPE: PRT
;    ORGANISM: human
US-10-277-966-2

  Query Match             95.4%;  Score 1322.5;  DB 14;  Length 234;
  Best Local Similarity   96.7%;  Pred. No. 1.9e-101;
  Matches  233;  Conservative    1;  Mismatches    0;  Indels    7;  Gaps    1;

Qy          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60

Qy         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120

Qy        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
```

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Qy        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
              ||||||||||||       |:||||||||||||||||||||||||||||||||||||||
Db        181 TSAQLGLHIWQL-------RKTQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 233

Qy        241 V 241
              |
Db        234 V 234


RESULT 12
US-10-264-237-1762
; Sequence 1762, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
;  APPLICANT: Birse et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PA131P1
;  CURRENT APPLICATION NUMBER: US/10/264,237
;  CURRENT FILING DATE:  2002-10-04
;  PRIOR APPLICATION NUMBER: PCT/US01/16450
;  PRIOR FILING DATE: 2001-05-18
;  PRIOR APPLICATION NUMBER: US 60/205,515
;  PRIOR FILING DATE: 2000-05-19
;  NUMBER OF SEQ ID NOS: 2876
;  SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1762
;   LENGTH: 246
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-264-237-1762

  Query Match             94.3%;  Score 1306.5;  DB 15;  Length 246;
  Best Local Similarity   92.1%;  Pred. No. 4.3e-100;
  Matches  233;  Conservative    1;  Mismatches    0;  Indels   19;  Gaps    2;

Qy          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60

Qy         61 Y------------PGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSF 108
              |            ||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YPAQLLGGWPVSCPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSF 120

Qy        109 GFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTV 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTV 180

Qy        169 VLLAVAACVLLLTSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGER 228
              ||||||||||||||||||||||       |:||||||||||||||||||||||||||||
Db        181 VLLAVAACVLLLTSAQLGLHIWQL-------RKTQLLLEVPPSTEDARSCQFPEEERGER 233

Qy        229 SAEEKGRLGDLWV 241
              |||||||||||||
Db        234 SAEEKGRLGDLWV 246


RESULT 13
US-09-915-593-6
; Sequence 6, Application US/09915593
; Patent No. US20020098525A1
; GENERAL INFORMATION:
;  APPLICANT: Ni, Jian
;  APPLICANT:  Ruben, Steven M.
;  TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
;  TITLE OF INVENTION:  TR11, TR11SV1, and TR11SV2
;  FILE REFERENCE: PF396P2
;  CURRENT APPLICATION NUMBER: US/09/915,593
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/221,577
;  PRIOR FILING DATE: 2000-07-28
;  PRIOR APPLICATION NUMBER: 09/512,363
;  PRIOR FILING DATE: 2000-02-23
;  PRIOR APPLICATION NUMBER: 60/144,076
;  PRIOR FILING DATE: 2000-07-16
;  PRIOR APPLICATION NUMBER: 60/134,172
;  PRIOR FILING DATE: 1999-05-13
;  PRIOR APPLICATION NUMBER: 60/121,648
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 09/176,200
;  PRIOR FILING DATE: 1998-10-21
;  PRIOR APPLICATION NUMBER: 60/063,212
;  PRIOR FILING DATE: 1997-10-21
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-915-593-6

  Query Match             92.0%;  Score 1274.5;  DB 9;  Length 240;
  Best Local Similarity   91.9%;  Pred. No. 1.9e-97;
  Matches  227;  Conservative    1;  Mismatches    0;  Indels   19;  Gaps    2;

Qy          7 MGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDY----- 61
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPAQLL 60

Qy         62 -------PGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCID 114
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGWPVSCPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCID 120

Qy        115 CASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVA 174
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVA 180

Qy        175 ACVLLLTSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKG 234
              ||||||||||||||||||       |:||||||||||||||||||||||||||||||||
Db        181 ACVLLLTSAQLGLHIWQL-------RKTQLLLEVPPSTEDARSCQFPEEERGERSAEEKG 233

Qy        235 RLGDLWV 241
              |||||||
Db        234 RLGDLWV 240


RESULT 14
US-10-283-105-6
; Sequence 6, Application US/10283105
; Publication No. US20030138426A1
; GENERAL INFORMATION:
;  APPLICANT: Ni, Jian
;  APPLICANT:  Ruben, Steven M
;  TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,
;  TITLE OF INVENTION:  TR11Sv22
;  FILE REFERENCE: PF396P3
;  CURRENT APPLICATION NUMBER: US/10/283,105
;  CURRENT FILING DATE:  2002-10-30
;  PRIOR APPLICATION NUMBER: 60/330,757
;  PRIOR FILING DATE: 2001-10-30
;  PRIOR APPLICATION NUMBER: 09/915,593
;  PRIOR FILING DATE: 2001-07-27
;  PRIOR APPLICATION NUMBER: 60/221,577
;  PRIOR FILING DATE: 2000-07-28
;  PRIOR APPLICATION NUMBER: 09/512,363
;  PRIOR FILING DATE: 2000-02-23
;  PRIOR APPLICATION NUMBER: 60/144,076
;  PRIOR FILING DATE: 1999-07-16
;  PRIOR APPLICATION NUMBER: 60/134,172
;  PRIOR FILING DATE: 1999-05-13
;  PRIOR APPLICATION NUMBER: 60/121,648
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 09/176,200
;  PRIOR FILING DATE: 1998-10-21
;  PRIOR APPLICATION NUMBER: 60/063,212
;  PRIOR FILING DATE: 1997-10-21
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;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: human
US-10-283-105-6

  Query Match             92.0%;  Score 1274.5;  DB 14;  Length 240;
  Best Local Similarity   91.9%;  Pred. No. 1.9e-97;
  Matches  227;  Conservative    1;  Mismatches    0;  Indels   19;  Gaps    2;

Qy          7 MGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDY----- 61
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPAQLL 60

Qy         62 -------PGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCID 114
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGWPVSCPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCID 120

Qy        115 CASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVA 174
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVA 180

Qy        175 ACVLLLTSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKG 234
              ||||||||||||||||||        |:|||||||||||||||||||||||||||||||||
Db        181 ACVLLLTSAQLGLHIWQL-------RKTQLLLEVPPSTEDARSCQFPEEERGERSAEEKG 233

Qy        235 RLGDLWV 241
              |||||||
Db        234 RLGDLWV 240


RESULT 15
US-10-277-966-6
; Sequence 6, Application US/10277966
; Publication No. US20030153499A1
; GENERAL INFORMATION:
;  APPLICANT: Ni, Jian
;  APPLICANT:  Ruben, Steven
;  TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,
;  TITLE OF INVENTION:  TR11SV2
;  FILE REFERENCE: PF396P1D1
;  CURRENT APPLICATION NUMBER: US/10/277,966
;  CURRENT FILING DATE:  2002-10-23
;  PRIOR APPLICATION NUMBER: 09/512,363
;  PRIOR FILING DATE: 2000-02-23
;  PRIOR APPLICATION NUMBER: 60/121,648
;  PRIOR FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: 60/134,172
;  PRIOR FILING DATE: 1999-05-13
;  PRIOR APPLICATION NUMBER: 60/144,076
;  PRIOR FILING DATE: 1999-07-16
;  PRIOR APPLICATION NUMBER: 09/176,200
;  PRIOR FILING DATE: 1998-10-21
;  PRIOR APPLICATION NUMBER: 60/063,212
;  PRIOR FILING DATE: 1997-10-21
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: human
US-10-277-966-6

  Query Match             92.0%;  Score 1274.5;  DB 14;  Length 240;
  Best Local Similarity   91.9%;  Pred. No. 1.9e-97;
  Matches  227;  Conservative    1;  Mismatches    0;  Indels   19;  Gaps    2;

Qy          7 MGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDY----- 61
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPAQLL 60

Qy         62 -------PGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCID 114
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGWPVSCPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCID 120

Qy        115 CASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVA 174
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVA 180

Qy        175 ACVLLLTSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKG 234
              ||||||||||||||||||        |:|||||||||||||||||||||||||||||||||
Db        181 ACVLLLTSAQLGLHIWQL-------RKTQLLLEVPPSTEDARSCQFPEEERGERSAEEKG 233

Qy        235 RLGDLWV 241
              |||||||
Db        234 RLGDLWV 240


Search completed: October 26, 2005, 16:11:21
Job time : 116.618 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 26, 2005, 15:38:30 ; Search time 25.693 Seconds
(without alignments)
902.513 Million cell updates/sec

Title: US-09-545-998B-4
Perfect score: 1386
Sequence: 1 MAQHGAMGAFRALCGLALLC.....EEERGERSAEEKGRLGDLWV 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	197	14.2	256	2	B32393	T-cell antigen 4-1
2	195.5	14.1	255	2	I38426	lymphocyte activat
3	175	12.6	272	2	I48700	gene ox40 protein
4	168.5	12.2	271	2	S12783	OX40 antigen precu
5	162	11.7	277	2	I37552	OX40 homolog - hum
6	144.5	10.4	305	2	A46476	B cell-associated
7	139	10.0	295	2	JC5559	lectin-B - Virgini
8	134.5	9.7	1801	1	MMRTS	laminin beta-2 cha
9	133	9.6	435	2	I54182	tumor necrosis fac
10	130.5	9.4	651	2	JC7705	death receptor-6 -
11	129	9.3	461	1	A35356	tumor necrosis fac
12	127.5	9.2	1574	2	T13954	MEGF6 protein - ra
13	124	8.9	277	2	A60771	B-cell activation
14	121.5	8.8	459	2	I48854	gene murine tumour
15	121	8.7	474	2	B38634	tumor necrosis fac
16	119.5	8.6	1798	2	S53869	laminin beta-2 cha
17	119	8.6	3635	2	T10053	laminin alpha 5 ch
18	118.5	8.5	1797	2	A55677	laminin beta-2 cha
19	117.5	8.5	1687	2	T30176	EGF repeat transme
20	115.5	8.3	1371	2	A33837	insulin-like growt
21	114.5	8.3	329	2	A48805	insulin-like growt
22	112	8.1	152	2	T18975	hypothetical prote
23	111	8.0	1111	2	T26972	hypothetical prote
24	111	8.0	2318	2	S45306	notch 3 protein -
25	110.5	8.0	2907	2	A57278	fibrillin-2 precur
26	110	7.9	1522	2	H88380	protein T22F7.3 [i
27	109.5	7.9	164	2	T24272	hypothetical prote
28	109.5	7.9	2531	2	A46019	notch-1 protein -
29	109	7.9	996	2	JE0237	apolipoprotein E r
30	108	7.8	540	2	B47417	insulin receptor-r
31	106.5	7.7	2918	2	A54105	fibrillin-2 precur
32	106	7.6	788	2	T25061	hypothetical prote
33	105.5	7.6	1113	2	JE0315	low-density lipopr
34	105.5	7.6	1251	2	A57293	latent transformin
35	105	7.6	188	2	T15651	hypothetical prote
36	105	7.6	1172	1	TSHUP2	thrombospondin 2 p
37	105	7.6	3566	1	A40701	tenascin-X precurs
38	104.5	7.5	2825	2	T14271	Doc4 protein, stre
39	103.5	7.5	1737	2	T00209	MEGF8 protein - hu
40	102.5	7.4	770	2	T00204	LDL receptor relat
41	102.5	7.4	770	2	T00203	LDL receptor-relat
42	102.5	7.4	956	1	A46016	thrombospondin 3 -
43	102	7.4	186	2	A28401	agglutinin isolect
44	102	7.4	1364	2	T00250	MEGF2 protein - hu
45	102	7.4	2871	2	A55567	fibrillin I - bovi

ALIGNMENTS

RESULT 1
B32393
T-cell antigen 4-1BB precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: B32393; I48879
R;Kwon, B.S.; Weissman, S.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989
A;Title: cDNA sequence of two inducible T-cell genes.
A;Reference number: A32393; MUID:89184547; PMID:2784565
A;Accession: B32393
A;Molecule type: mRNA
A;Residues: 1-256 <KWO>
A;Cross-references: UNIPROT:P20334; GB:J04492; NID:g201121; PIDN:AAA40167.1; PID:g201122
R;Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Pickard, R.T.
J. Immunol. 152, 2256-2262, 1994
A;Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1BB.
A;Reference number: I48879; MUID:94179805; PMID:8133039
A;Accession: I48879
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-256 <RES>
A;Cross-references: EMBL:U02567; NID:g1117783; PIDN:AAA93113.1; PID:g409178
C;Genetics:
A;Introns: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: transmembrane protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-256/Product: 4-1BB protein #status predicted <MAT>

Query Match 14.2%; Score 197; DB 2; Length 256;
Best Local Similarity 28.8%; Pred. No. 2.9e-08;
Matches 64; Conservative 25; Mismatches 85; Indels 48; Gaps 10;

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Qy          34 CGPGRL-LLGTGTDARCCRVHTTRCCRDYPGEECCSEW---DCMCVQPEFHCGDPCCTTC 89
               | |    :|   :   |||    |   :  :: ||     :| |::  |||  | || |
Db          47 CPPSTFSSIGGQPNCNICRV----CAGYFRFKKFCSSTHNAECECIE-GFHCLGPQCTRC 101

Qy          90 RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGH-EGHCKPWTDCTQFGFLTVFPGNKT 148
                 | ||| :  ||       |  |: |||:  :  | |:|||:|:  |   :  |
Db         102 -EKDCRPGQELTKQG-------CKTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTE 153

Qy         149 HNAVCVP---------------GSPPAEPLGWLTVVLLAVAACVLLLTSAQLGLHIWQL 192
               : || |               | |    |  ||: |   :| :| |      : |  |
Db         154 KDVVCGPPVVSFSPSTTISVTPEGGPGGHSLQVLTLFLALTSALLLAL------IFITLL 207

Qy         193 RSQCMWPRETQLLLEVPP--------STEDARSCQFPEEERG 226
                |   | |:    :   |           ||| ||: |:|| |
Db         208 FSVLKWIRKKFPHIFKQPFKKTTGAAQEEDACSCRCPQEEEG 249
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RESULT 2

```
I38426
lymphocyte activation-induced receptor ILA precursor - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I38426; JT0752
R;Alderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk, B.; R
Eur. J. Immunol. 24, 2219-2227, 1994
A;Title: Molecular and biological characterization of human 4-1BB and its ligand.
A;Reference number: I38426; MUID:94374434; PMID:8088337
A;Accession: I38426
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-255 <RES>
A;Cross-references: UNIPROT:Q07011; EMBL:U03397; NID:g571320; PIDN:AAA53133.1; PID:g5713
R;Schwarz, H.; Tuckwell, J.; Lotz, M.
Gene 134, 295-298, 1993
A;Title: A receptor induced by lymphocyte activation (ILA): a new member of the human ne
A;Reference number: JT0752; MUID:94085794; PMID:8262389
A;Accession: JT0752
A;Molecule type: mRNA
A;Residues: 1-106,'R',108-255 <SCH>
C;Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-necro
C;Comment: This receptor recongnizes soluble, cell-surface bound or extracellular matrix
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-255/Product: lymphocyte activation-induced receptor ILA #status predicted <MAT>
F;187-213/Domain: transmembrane #status predicted <TMM>
F;138,149/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;234,235/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predict
F;242/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

  Query Match             14.1%;  Score 195.5;  DB 2;  Length 255;
  Best Local Similarity   28.8%;  Pred. No. 3.8e-08;
  Matches   66;  Conservative   21;  Mismatches   81;  Indels   61;  Gaps   12;

Qy         34 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG-----EECCS----EWDCMCVQPEFHCGDP 84
              | |      |   | | :     ||   |     :|| |    | ||     | |||
Db         48 CPPNSFSSAGG--QRTCDI-----CRQCKGVFRTRKECSSTSNAECDC---TPGFHCLGA 97

Qy         85 CCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFP 144
              |: |    |  || :  :|       | ||  |||:    | |:|||:|:  |   :
Db         98 GCSMC-EQDCKQGQELTKKG-------CKDCCFGTFNDQKRGICRPWTNCSLDGKSVLVN 149

Qy        145 GNKTHNAVCVPG-----------SPPA---EPLGWLTVV--LLAVAACVLLLTSAQLGLH 188
              | |  : || |            :|||   ||      ::   ||: :  ||      | |
Db        150 GTKERDVVCGPSPADLSPGASSVTPPAPAREPGHSPQIISFFLALTSTALLFLLFFLTLR 209

Qy        189 -----------IWQLRSQCMWPRETQLLLEVPPSTEDARSCQPPEEERG 226
                        ::  :   | | :|          ||  ||:||||| |
Db        210 FSVVKRGRKKLLYIFKQPFMRPVQT-------TQEEDGCSCRFPEEEEG 251


RESULT 3
I48700
gene ox40 protein - mouse
N;Alternate names: OX40 antigen
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48700; I48334; S34377
R;Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.;
J. Immunol. 151, 5261-5271, 1993
A;Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell int
A;Reference number: I48700; MUID:94044750; PMID:8228223
A;Accession: I48700
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-272 <RES>
A;Cross-references: UNIPROT:P47741; EMBL:Z21674; NID:g312827; PIDN:CAA79772.1; PID:g3128
R;Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
Eur. J. Immunol. 25, 926-930, 1995
A;Title: Gene structure and chromosomal localization of the mouse homologue of rat OX40
A;Reference number: I48334; MUID:95255413; PMID:7737295
A;Accession: I48334
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-14,'G',16-272 <RE2>
A;Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819
C;Genetics:
A;Gene: ox40
A;Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C;Superfamily: CD27 antigen; NGF receptor repeat homology

  Query Match             12.6%;  Score 175;  DB 2;  Length 272;
  Best Local Similarity   26.7%;  Pred. No. 1.6e-06;
  Matches   58;  Conservative   19;  Mismatches   70;  Indels   70;  Gaps   10;

Qy         39 LLLGTGTDAR--CCRVHT----TRCCRD-YPG----EECCSEWDCMCVQPEFHCGDPC-- 85
              | |  |  ||   |  ||      :|||:  ||       |    | :|         ||
Db         14 LALTLGVTARRLNCVKHTYPSGHKCCRECQPGHGMVSRCDHTRDTLC--------HPCET 65

Qy         86 --------------CTTCRHHP-----------------CPPGQGVQSQGKFSFGFQCID 114
                           || | |                  | ||    :    :  | |:
Db         66 GFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVCRCRPGTQPRQDSGYKLGVDCVP 125

Qy        115 CASGTFSGGHEGHCKPWTDCTQFGFLTVPPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVA 174
              |  | || |:   |||||:||  |  |  | : : :|||   |           |||
Db        126 CPPGHFSPGNNQACKPWTNCTLSGKQTRHPASDSLDAVCEDRS-----------LLA-- 171

Qy        175 ACVLLLTSAQLGLHIWQLRSQCMWPRETQLLLEVPPS 211
                ||  : :       ::|  :||| ::  |  ||:
Db        172 --TLLWETQRPTFRPTTVQSTTVWPRTSE--LPSPPT 204


RESULT 4
S12783
OX40 antigen precursor - rat
N;Alternate names: nerve growth factor receptor homolog
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: S12783; S08036
R;Mallett, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A;Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes
A;Reference number: S12783; MUID:90214614; PMID:2157591
A;Accession: S12783
A;Molecule type: mRNA
A;Residues: 1-271 <MAL>
A;Cross-references: UNIPROT:P15725; EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: growth factor receptor; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-271/Product: OX40 antigen #status predicted <MAT>
F;211-235/Domain: transmembrane #status predicted <TMM>

  Query Match             12.2%;  Score 168.5;  DB 2;  Length 271;
  Best Local Similarity   27.7%;  Pred. No. 4.9e-06;
  Matches   62;  Conservative   17;  Mismatches   80;  Indels   65;  Gaps   11;

Qy         26 QRPTGGPGCGPGRLLLG--TGTDARCCRVHTT-----RCCRD-YPGEECCSEWD------ 71
              |:||         ||||   |   :   |  |      :|||:  ||    |  |
Db          6 QQPT-------AFLLLGLSLGVTVKLNCVKDTYPSGHKCCRECQPGHGMVSRCDHTRDTV 58

Qy         72 CMCVQPEFHCG----DPC--CTTCRHH-----------------PCPPGQGVQSQGKFSF 108
              |   :| |:      | |  || | |                 | ||    :
Db         59 CHPCEPGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTEDTVCQCRPGTQPRQDSSHKL 118

Qy        109 GFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTV 168
              |  |: |  | || |     |||||:||  |     | : : : ||   |
Db        119 GVDCVPCPPGHFSPGSNQACKPWTNCTLSGKQIRHPASNSLDTVCEDRS---------- 167

Qy        169 VLLAVAACVLLLTSAQLGLHIWQLRSQCMWPRETQLLLEVPPST 212
               |||     ||  : :       : |  :||| :||     |||
Db        168 -LLA----TLLWETQRTTFRPTTVPSTTVWPRTSQL-----PST 201
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```
RESULT 5
I37552
OX40 homolog - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I37552
R;Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat
Eur. J. Immunol. 24, 677-683, 1994
A;Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment c
A;Reference number: I37552; MUID:94170844; PMID:7510240
A;Accession: I37552
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-277 <RES>
A;Cross-references: UNIPROT:P43489; EMBL:X75962; NID:g472957; PIDN:CAA53576.1; PID:g4729
C;Superfamily: CD27 antigen; NGF receptor repeat homology

  Query Match             11.7%;  Score 162;  DB 2;  Length 277;
  Best Local Similarity   29.7%;  Pred. No. 1.6e-05;
  Matches   51;  Conservative   11;  Mismatches   92;  Indels   18;  Gaps    5;

Qy          5 GAMGAFRALCGLALLCALSLG----------QRPTGGPGCGPGRLLLGTGTDARCCRVHT 54
              ||     |  |   ||  | ||           |:    |   |   | |  :|| |
Db          4 GARRLGRGPCAALLLLGLGLSTVTGLHCVGDTYPSNDRCCHECR--PGNGMVSRCSRSQN 61

Qy         55 TRCCRDYPG--EECCSEWDCM-CVQPEFHCGD---PCCTTCRHHPCPPGQGVQSQGKFSF 108
              | |    ||   :  |   |  |       ||  :   |     | |    :
Db         62 TVCRPCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSYKP 121

Qy        109 GFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPA 160
              |  |  |  | || |    |||||:||  |  |: | : : :|:|    |||
Db        122 GVDCAPCPPGHFSPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPA 173


RESULT 6
A46476
B cell-associated surface molecule CD40, long splice form - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46476; A46515
R;Torres, R.M.; Clark, E.A.
J. Immunol. 148, 620-626, 1992
A;Title: Differential increase of an alternatively polyadenylated mRNA species of murine
A;Reference number: A46476; MUID:92105763; PMID:1370315
A;Accession: A46476
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-305 <TOR>
A;Cross-references: UNIPROT:P27512; GB:M83312; NID:g1553058
A;Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)
A;Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0
R;Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne,
J. Immunol. 149, 3921-3926, 1992
A;Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A;Reference number: A46515; MUID:93094586; PMID:1281194
A;Accession: A46515
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-287,'LV' <GRI>
A;Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126; N
A;Experimental source: BALB/c, liver
A;Note: sequence extracted from NCBI backbone (NCBIP:120357)
C;Comment: For an alternative splice form, see PIR:A46515.
C;Comment: For an alternative splice form, see PIR:A46476.
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: alternative splicing; transmembrane protein
F;105-144/Domain: NGF receptor repeat homology <NGF>

  Query Match             10.4%;  Score 144.5;  DB 2;  Length 305;
  Best Local Similarity   22.8%;  Pred. No. 0.00039;
  Matches   65;  Conservative   27;  Mismatches  104;  Indels   89;  Gaps   12;

Qy         13 LCGL--ALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCC-------------------- 50
              || |   || |: |||  |    |   : |      | :||
Db          7 LCALWGCLLTAVHLGQCVT----CSDKQYL----HDGQCCDLCQPGSRLTSHCTALEKTQ 58

Qy         51 ----------------RVHTTRCCRDYPG----EECCSEWDCMCVQPE-FHCGDPCCTT 88
                             | |  | |    |    :|  :| | :|   |  ||    |
Db         59 CHPCDSGEFSAQWNREIRCHQHRHCEPNQGLRVKKEGTAESDTVCTCKEGQHCTSKDCEA 118

Qy         89 C-RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE--GHCKPWTDCTQFGFLTVFPG 145
              | :| || || ||      :    |  |  | ||         | ||| |       :  |
Db        119 CAQHTPCIPGFGVMEMATETTDTVCHPCPVGFFSNQSSLFEKCYPWTSCEDKNLEVLQKG 178

Qy        146 NKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQLGLHIWQLRSQCMWPRETQLL 205
                | :|   |        :  :|:      :|:|   : |:| ::  :   |:: ::|
Db        179 TSQTNVICGLKSR-------MRALLVIPVVMGILITIFGVFLYIKKVVKK---PKDNEML 228

Qy        206 LEVPPST--------------------EDARSCQFPEEERGERS 229
                ||:                     |   ||   :| |: |
Db        229 ---PPAARRQDPQEMEDYPGHNTAAPVQETLHGCQPVTQEDGKES 270


RESULT 7
JC5559
lectin-B - Virginian pokeweed
C;Species: Phytolacca americana (Virginian pokeweed)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
C;Accession: JC5559
R;Yamaguchi, K.; Yurino, N.; Kino, M.; Ishiguro, M.; Funatsu, G.
Biosci. Biotechnol. Biochem. 61, 690-698, 1997
A;Title: The amino acid sequence of mitogenic lectin-B from the roots of pokeweed (Phyto]
A;Reference number: JC5559; MUID:97290889; PMID:9145528
A;Accession: JC5559
A;Molecule type: protein
A;Residues: 1-295 <YAM>
A;Cross-references: UNIPROT:Q9AVB0
A;Experimental source: root
C;Comment: This protein is a lectin specific for N-acetylglucosamine-containing saccharide
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pla
C;Keywords: glycoprotein
F;96,139/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             10.0%;  Score 139;  DB 2;  Length 295;
  Best Local Similarity   28.8%;  Pred. No. 0.001;
  Matches   36;  Conservative   18;  Mismatches   41;  Indels   30;  Gaps    8;

Qy         20 CALSLGQRPTGGP-------GCGPGRLLLGTGTDARCCRVHTTRCCRDYPG-----EECC 67
              | :  | |             ||      | |  ::|   :  || :|: |     : ||
Db        133 CGVDFGNRTCPNDLCCSEWGWCGITEGYCGEGCQSQC---NHQRCGKDFAGRTCLNDLCC 189

Qy         68 SEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQ-C---IDCASGTFSGG 123
              |||   |   | |||  | : | :: |         |: :|||: |   : |:|| : |
Db        190 SEWG-WCGSSEAHCGQGCQSNCNYNRC---------GR-NFGFRTCPNELCCSSGGWCGS 238

Qy        124 HEGHC 128
                :: ||
Db        239 NDAHC 243


RESULT 8
MMRTS
laminin beta-2 chain precursor - rat
N;Alternate names: laminin chain B3; S-laminin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: S03539
R;Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.
Nature 338, 229-234, 1989
A;Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the neurom
A;Reference number: S03539; MUID:89159410; PMID:2922051
A;Accession: S03539
A;Molecule type: mRNA
A;Residues: 1-1801 <HUN>
A;Cross-references: UNIPROT:P15800; EMBL:X16563; NID:g57250; PIDN:CAA34561.1; PID:g57251
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin c
```

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C;Function:
A;Description: interact with cells and with other basement membrane proteins to promote
C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular
F;1-35/Domain: signal sequence #status predicted <SIG>
F;36-1801/Product: laminin beta-2 chain #status predicted <MAT>
F;36-285/Domain: VI <DOM6>
F;286-555/Domain: V <DOM5>
F;286-347/Domain: laminin-type EGF-like homology <LE01>
F;350-410/Domain: laminin-type EGF-like homology <LE02>
F;413-470/Domain: laminin-type EGF-like homology <LE03>
F;473-522/Domain: laminin-type EGF-like homology <LE04>
F;525-555/Domain: laminin-type EGF-like homology #status atypical <LE05>
F;556-784/Domain: IV <DOM4>
F;786-831/Domain: laminin-type EGF-like homology <LE06>
F;788-1196/Domain: III <DOM3>
F;834-877/Domain: laminin-type EGF-like homology <LE07>
F;880-927/Domain: laminin-type EGF-like homology <LE08>
F;930-986/Domain: laminin-type EGF-like homology <LE09>
F;989-1038/Domain: laminin-type EGF-like homology <LE10>
F;1041-1095/Domain: laminin-type EGF-like homology <LE11>
F;1098-1143/Domain: laminin-type EGF-like homology <LE12>
F;1146-1190/Domain: laminin-type EGF-like homology <LE13>
F;1197-1412/Domain: II <DOM2>
F;1197-1412/Region: heptad repeats
F;1413-1445/Domain: alpha <ALP>
F;1446-1801/Region: heptad repeats
F;1446-1801/Domain: I <DOM1>
F;45-50/Disulfide bonds: #status predicted
F;251,371,1088,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #status p
F;1193,1196,1800/Disulfide bonds: interchain #status predicted

  Query Match              9.7%;  Score 134.5;  DB 1;  Length 1801;
  Best Local Similarity   26.9%;  Pred. No. 0.0088;
  Matches   63;  Conservative    6;  Mismatches   60;  Indels  105;  Gaps   15;

Qy          8 GAFRALC-GLALLCALSLG---------QRPTGG-PGCGP----GRLLLGTGTDARCCRV 52
              ||  ||| | :  |    |          ||   | | | |    ||         |  |
Db        840 GALSALCEGTSGQCLCRTGAFGLRCDHCQRGQWGFPNCRPCVCNGR--------ADECDA 891

Qy         53 HTTRC--CRDYPGEECCSEWDCMCVQPEFHCGDPCCT---TCRHHPCPPGQGVQSQGKFS 107
              ||  |  |||| | | |       |:   || |||        ||  ||| | |  ||  |:
Db        892 HTGACLGCRDYTGGEHCER----CI-AGFH-GDPRLPYGGQCRPCPCPEGPG--SQRHFA 943

Qy        108 --------------------FGFQCIDCASGTF-------------------------- 120
                                  | :|  || | |
Db        944 TSCHRDGYSQQIVCHCRAGYTGLRCEACAPGHFGDPSKPGGRCQLCECSGNIDPTDPGAC 1003

Qy        121 --------------SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC-VPGSPP 159
                          | | |||||       ||         |   | : |: |
Db       1004 DPHTGQCLRCLHHTEGPHCGHCKP-------GFHGQAARQSCHRCTCNLLGTDP 1050


RESULT 9
I54182
tumor necrosis factor receptor 2-related protein - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C;Accession: I54182
R;Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A;Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen
A;Reference number: I54182; MUID:93252381; PMID:8486360
A;Accession: I54182
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-435 <RES>
A;Cross-references: UNIPROT:P36941; GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762
C;Genetics:
A;Gene: GDB:LTBR
A;Cross-references: GDB:1230195; OMIM:600979
A;Map position: 12p13.3-12p13.1
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolo

  Query Match              9.6%;  Score 133;  DB 2;  Length 435;
  Best Local Similarity   25.0%;  Pred. No. 0.004;
  Matches   57;  Conservative   17;  Mismatches   86;  Indels   68;  Gaps   13;

Qy         34 CGPGRLLLGTGTDARCCRVHTTRC----------------------CRDYPGEE----C 66
              | |     ||   |:| |:  | |                          |    | |    |
Db         62 CPP-----GTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICQLCRPCDPVMGLEEIAPC 116

Qy         67 CS--EWDCMCVQPEFHCGDPC--CTTCR-HHPCPPGQGVQSQGKFSFG-FQCIDCASGTF 120
              |  :  | | ||   |      || |     ||||   : : :    |   |: | :| |
Db        117 TSKRKTQCRC-QPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNNHCVPCKAGHF 175

Qy        121 --SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG-------WLTVVLL 171
                :      |:| | |   | :   ||    :  |     | |||         :  |||
Db        176 QNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTC---KNPLEPLPPEMSGTMLMLAVLL 232

Qy        172 AVAACVLLLTSAQLGLHIWQLRSQCMWPRETQL------LLEVPPSTE 213
                :|  :|| |                |:|      |      ||:  |  |
Db        233 PLAFFLLLATV-----------FSCIWKSHPSLCRKLGSLLKRRPQGE 269


RESULT 10
JC7705
death receptor-6 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Jul-2004
C;Accession: JC7705
R;Bridgham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
A;Title: Conservation of death receptor-6 in avian and piscine vertebrates.
A;Reference number: JC7705; MUID:21308433; PMID:11414698
A;Accession: JC7705
A;Molecule type: mRNA
A;Residues: 1-651 <BRI>
A;Cross-references: UNIPROT:Q98SM6; GB:AF349908
C;Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs
tresia, activates a cell death and/or survival signaling cascade.
C;Genetics:
A;Gene: dr-6
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolo
C;Keywords: ovary
F;1-21/Domain: signal sequence #status predicted <SIG>
F;52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>
F;332-350/Domain: transmembrane #status predicted <TMM>
F;410-475/Domain: death domain #status predicted <DED>
F;551-651/Region: conserved cytoplasmic #status predicted

  Query Match              9.4%;  Score 130.5;  DB 2;  Length 651;
  Best Local Similarity   29.8%;  Pred. No. 0.0084;
  Matches   39;  Conservative   14;  Mismatches   55;  Indels   23;  Gaps    6;

Qy         48 RC--CR-------VHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQ 98
              ||  ||       :  | |          :: :| |:   |   | |     :  || |
Db         90 RCHPCRKPCELPMIEKTHC-------TALTDRECTCLSGTFQINDTCVP---YTVCPVGW 139

Qy         99 GVQSQGKFSFGFQCIDCASGTFSGGHEG--HCKPWTDCTQFGFLTVFPGNKTHNAVCVPG 156
              ||: :|  :   :|  |  ||||        || :|||      : | || |  : ||
Db        140 GVRKKGTETEDVRCKPCLRGTFSDVPSSVMKCKTYTDCFGKNMVVVKPGTKESDNVC--X 197

Qy        157 SPPAEPLGWLT 167
              || : |   ||
Db        198 SPASLPNTSLT 208


RESULT 11
A35356
tumor necrosis factor receptor 2 precursor [validated] - human
N;Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094
R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K.
```

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Science 248, 1019-1023, 1990
A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular and
A;Reference number: A35356; MUID:90260639; PMID:2160731
A;Accession: A35356
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-461 <SMI>
A;Cross-references: UNIPROT:P20333; GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186
R;Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires,
Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
A;Title: A second tumor necrosis factor receptor gene product can shed a naturally occur
A;Reference number: A36475; MUID:91045991; PMID:2172983
A;Accession: A36475
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-195,'R',197-461 <KOH>
A;Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
R;Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.
Cytokine 2, 231-237, 1990
A;Title: Two human TNF receptors have similar extracellular, but distinct intracellular,
A;Reference number: A48416; MUID:91370690; PMID:1966549
A;Accession: A48416
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 23-461 <DEM>
A;Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649
A;Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBIP:63371)
R;Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A;Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra
A;Reference number: A36007; MUID:90349572; PMID:2166946
A;Accession: A36007
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 116-140,'P',142-195,'R',197-362,'T',364-461 <HEL>
A;Cross-references: GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:g339752
R;Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
J. Biol. Chem. 265, 20131-20138, 1990
A;Title: Purification and partial amino acid sequence analysis of two distinct tumor nec
A;Reference number: A23666; MUID:91056048; PMID:2173696
A;Accession: A23666
A;Status: preliminary
A;Molecule type: protein
A;Residues: 23-40;65-69;136-141;300-306 <LOE>
R;Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A;Reference number: A35010; MUID:90110215; PMID:2153136
A;Accession: B35010
A;Status: preliminary
A;Molecule type: protein
A;Residues: 27-31 <ENG>
R;Kuhnert, P.; Kemper, O.; Wallach, D.
Gene 150, 381-386, 1994
A;Title: Cloning, sequencing and partial functional characterization of the 5' region of
A;Reference number: I38094; MUID:95121934; PMID:7821811
A;Accession: I38094
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-37 <RES>
A;Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701
C;Genetics:
A;Gene: GDB:TNFR2
A;Cross-references: GDB:125914; OMIM:191191
A;Map position: 1p36.2-1p36.2
A;Introns: 26/3
A;Note: the list of introns is incomplete
C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolo
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
F;40-76/Domain: NGF receptor repeat homology <NG1>
F;78-119/Domain: NGF receptor repeat homology <NG2>
F;120-162/Domain: NGF receptor repeat homology <NG3>
F;164-201/Domain: NGF receptor repeat homology <NG4>
F;262-279/Domain: transmembrane #status predicted <TMN>
F;280-461/Domain: intracellular #status predicted <INT>
F;171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             9.3%;  Score 129;  DB 1;  Length 461;
  Best Local Similarity   22.4%;  Pred. No. 0.0085;
  Matches   63;  Conservative   27;  Mismatches   81;  Indels  110;  Gaps   15;

Qy         34 CGPG---RLLLGTGTDARC----------------CRVHTTRCCRDYPGEECCSEWD-- 71
                ||    ::     :|  |                |    :||  |    : |:
Db         57 CSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNR 116

Qy         72 -CMCVQPEFHC------GDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSG-- 122
               | | :| ::|       |    |    |   | || ||   |  :    |  || ||||
Db        117 ICTC-RPGWYCALSKQEGCRLCAPLR--KCRPGFGVARPGTETSDVVCKPCAPGTFSNTT 173

Qy        123 GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC---------VPG----------------- 156
                  |:|   |     :   ||| : :|||          ||
Db        174 SSTDICRPHQICN----VVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVSTRSQHTQP 229

Qy        157 -----------------SPPAE--------PLGW------LTVVLLAVAACVLLLTSAQ 184
                              |||||         |:|       | :::: |  ||::
Db        230 TPEPSTAPSTSFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLIIGVVNCVIMT---- 285

Qy        185 LGLHIWQLRSQCMWPRETQLLLEVPPSTED-ARSCQFPEEE 224
                  |:: :   |   |   :||    | ||  | ||::
Db        286 ------QVKKK---PLCLQREAKVPHLPADKARGTQGPEQQ 317


RESULT 12
T13954
MEGF6 protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13954
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs i
A;Reference number: Z14126; MUID:98360089; PMID:9693030
A;Accession: T13954
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1574 <NAK>
A;Cross-references: UNIPROT:O88281; EMBL:AB011532; NID:g3449293; PIDN:BAA32462.1; PID:g3
A;Experimental source: strain Sprague-Dawley; brain
C;Genetics:
A;Gene: MEGF6

  Query Match             9.2%;  Score 127.5;  DB 2;  Length 1574;
  Best Local Similarity   27.7%;  Pred. No. 0.028;
  Matches   53;  Conservative   12;  Mismatches   65;  Indels   61;  Gaps   11;

Qy         45 TDARCCRVHTTRCCRDY---PGEE-CCSEWDCMCVQPEFHCGDPCCTT-----CRHHPCP 95
              |:||       |||  :   ||:| | |: | |       |  |||  |     ||   ||
Db         99 TEART----VFRCCPGWSQKPGQEGCLSDVD-ECASANGGCEGPCCNTVGGFYCR---CP 150

Qy         96 PGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVP 155
              ||  :| ||          |       | | |:                    |  | |
Db        151 PGYQLQGDGK--------TCQDVDECRAHNGGCQ------------------HRCVNTP 183

Qy        156 GS-----PPAEPLGWLTVVLLAVAACVLLLTSAQ---LGLHIWQLRSQCMWPRETQLLLE 207
              ||      |   |        ||:::| |      |   : | : | | ||    : |
Db        184 GSYLCECKPGFRLHTDGRTCLAISSCTLGNGGCQHQCVQLTVTQHRCQCRPQYQLQ---- 239

Qy        208 VPPSTEDARSC 218
                 || | |
Db        240 -----EDGRRC 245


RESULT 13
A60771
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B-cell activation protein CD40 precursor - human
N;Alternate names: B-cell surface antigen Bp50
C;Species: Homo sapiens (man)
C;Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: S04460; A60771
R;Stamenkovic, I.; Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A;Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor
A;Reference number: S04460; MUID:89356608; PMID:2475341
A;Accession: S04460
A;Molecule type: mRNA
A;Residues: 1-277 <STA>
A;Cross-references: UNIPROT:P25942; EMBL:X60592; NID:g29850; PIDN:CAA43045.1; PID:g29851
R;Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A;Title: Biochemical characteristics and partial amino acid sequence of the receptor-lik
A;Reference number: A60771; MUID:89093941; PMID:2463309
A;Accession: A60771
A;Molecule type: protein
A;Residues: 21-50 <BRA>
A;Experimental source: Burkitt lymphoma cell line Raji
C;Genetics:
A;Gene: GDB:CD40
A;Cross-references: GDB:215268; OMIM:109535
A;Map position: 20q12-20q13.2
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
F;21-193/Domain: extracellular #status predicted <EXT>
F;194-215/Domain: transmembrane #status predicted <TMM>
F;216-277/Domain: intracellular #status predicted <CYT>
F;153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             8.9%;  Score 124;  DB 2;  Length 277;
  Best Local Similarity   23.7%;  Pred. No. 0.014;
  Matches   51;  Conservative   21;  Mismatches  117;  Indels   26;  Gaps    8;

Qy          34 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG----EECCSEWDCMCVQPE-FHCGDPCCTT 88
               ||    |    :  |   |  : |    |    ::  || | :|   | :||    | :
Db          62 CGESEFLDTWNRETHC---HQHKYCDPNLGLRVQQKGTSETDTICTCEEGWHCTSEACES 118

Qy          89 C-RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEG--HCKPWTDCTQFGFLTVFPG 145
               |  |  | || ||:          |  |  | ||        | ||| |     :    |
Db         119 CVLHRSCSPGFGVKQIATGVSDTICEPCPVGFFSNVSSAFEKCHPWTSCETKDLVVQQAG 178

Qy         146 NKTHNAVCVPGSPPAEPLGWLTV--VLLAVAACVLLL---------TSAQLGLHIWQLRS 194
                 : ||      | : |  | |  ::  :   :||:                |  |
Db         179 TNKTDVVC----GPQDRLRALVVIPIIFGILFAILLVLVFIKKVAKKPTNKAPHPKQEPQ 234

Qy         195 QCMWPRETQLLLEVPPSTEDARSCQFPEEEERGERS 229
               :  :| :        |  |    ||   :| |: |
Db         235 EINFPDDLPGSNTAAPVQETLHGCQPVTQEDGKES 269


RESULT 14
I48854
gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48854
R;Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A;Reference number: I48854; MUID:95178848; PMID:7873884
A;Accession: I48854
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-459 <RES>
A;Cross-references: UNIPROT:Q62327; EMBL:X76401; NID:g433830; PIDN:CAA53981.1; PID:g4338
C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolo
F;151-188/Domain: NGF receptor repeat homology <NGF>

  Query Match             8.8%;  Score 121.5;  DB 2;  Length 459;
  Best Local Similarity   21.0%;  Pred. No. 0.032;
  Matches   60;  Conservative   29;  Mismatches   96;  Indels  101;  Gaps   12;

Qy          48 RCCRVHTTRCCRDYPGEECCSEWD---CMCVQPEF-----HCGDPCCTTC-RHHPCPPGQ 98
               | |   :: |  |       |::     | |    :     | |   |  | |   | ||
Db          77 RTCLSCSSSCSTDQVETRACTKQQNRVCACEAGRYCALKTHSGS--CRQCMRLSKCGPGF 134

Qy          99 GVQSQGKFSFGFQCIDCASGTFSG--GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPG 156
               || |    :    |  || ||||        |:|   |:    :   ||| : :||| |
Db         135 GVASSRAPNGNVLCKACAPGTFSDTTSSTDVCRPHRICS----ILAIPGNASTDAVCAPE 190

Qy         157 SP--------------------------PAE-----------------------PLGW 165
               ||                        |::                       |:|
Db         191 SPTLSAIPRTLYVSQPEPTRSQPLDQEPGPSQTPSILTSLGSTPIIEQSTKGGISLPIGL 250

Qy         166 ------LTVVLLAVAACVLLLTSAQLGL---------HIWQLRSQCMWPRETQLLLEVPP 210
                   | :::| :  | :|:   :             |:   :||     | | ||   |
Db         251 IVGVTSLGLLMLGLVNCFILVQRKKKPSCLQRDAKVPHVPDEKSQDAVGLEQQHLLTTAP 310

Qy         211 STE-----------DARS-------CQFPEEERGERSAEEKGRLGD 238
               |:           | |:       :   | :| : |    |: |
Db         311 SSSSSSLESSASAGDRRAPPGGHPQARVMAEAQGSQEARASSRISD 356


RESULT 15
B38634
tumor necrosis factor receptor type 2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: B38634; A40254; S54816
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.Y
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor re
A;Reference number: A38634; MUID:91187885; PMID:1849278
A;Accession: B38634
A;Molecule type: mRNA
A;Residues: 1-474 <LEW>
A;Cross-references: UNIPROT:P25119; GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenki
Mol. Cell. Biol. 11, 3020-3026, 1991
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for t
A;Reference number: A40254; MUID:91246168; PMID:1645445
A;Accession: A40254
A;Molecule type: mRNA
A;Residues: 1-474 <GOO>
A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R;Kissonerghis, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y.
submitted to the EMBL Data Library, May 1995
A;Description: Characterization of the promoter region of the murine p75-TNF receptor.
A;Reference number: S54816
A;Accession: S54816
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-22 <KIS>
A;Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044
C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolog
C;Keywords: cytokine receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
F;40-77/Domain: NGF receptor repeat homology <NG1>
F;79-120/Domain: NGF receptor repeat homology <NG2>
F;166-203/Domain: NGF receptor repeat homology <NG4>

  Query Match             8.7%;  Score 121;  DB 2;  Length 474;
  Best Local Similarity   21.1%;  Pred. No. 0.036;
  Matches   59;  Conservative   27;  Mismatches   92;  Indels  102;  Gaps   11;

Qy          46 DARCCRVHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTC-RHHPCPPGQGVQSQG 104
               : | |     | |     |  |           : | |   |  | |   | || || |
Db         107 EIRACTKQQNRVCACEAGRYCAL---------KTHSGS--CRQCMRLSKCGPGFGVASSR 155

Qy         105 KFSFGFQCIDCASGTFSG--GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSP---- 158
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                :    |  || ||||        |:|   |:    :   ||| : :||| | ||
Db        156 APNGNVLCKACAPGTFSDTTSSTDVCRPHRICS----ILAIPGNASTDAVCAPESPTLSA 211

Qy        159 ----------------------PAE-----------------------PLGW------ 165
                                     |::                       |:|
Db        212 IPRTLYVSQPEPTRSQPLDQEPGPSQTPSILTSLGSTPIIEQSTKGGISLPIGLIVGVTS 271

Qy        166 LTVVLLAVAACVLLLTSAQLGL---------HIWQLRSQCMWPRETQLLLEVPPSTE--- 213
                | :::| :  |::|:   :           |:   :||    | | ||   ||:
Db        272 LGLLMLGLVNCIILVQRKKKPSCLQRDAKVPHVPDEKSQDAVGLEQQHLLTTAPSSSSSS 331

Qy        214 --------DARS-------CQFPEEERGERSAEEKGRLGD 238
                      | |:        :   | :| : |    |: |
Db        332 LESSASAGDRRAPPGGHPQARVMAEAQGFQEARASSRISD 371
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Search completed: October 26, 2005, 15:52:34
Job time : 26.693 secs

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 26, 2005, 15:29:08 ; Search time 118.701 Seconds
(without alignments)
1039.676 Million cell updates/sec

Title: US-09-545-998B-4
Perfect score: 1386
Sequence: 1 MAQHGAMGAFRALCGLALLC.....EEERGERSAEEKGRLGDLWV 241

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1386	100.0	241	1	TR18_HUMAN	Q9y5u5 homo sapien
2	735.5	53.1	228	1	TR18_MOUSE	O35714 mus musculu
3	735.5	53.1	250	2	Q8C4K3	Q8c4k3 mus musculu
4	202	14.6	275	2	Q80WM9	Q80wm9 mus musculu
5	201.5	14.5	276	2	Q71F55	Q71f55 mus musculu
6	197	14.2	256	1	TNR9_MOUSE	P20334 mus musculu
7	195.5	14.1	255	1	TNR9_HUMAN	Q07011 homo sapien
8	191	13.8	270	2	Q75SV8	Q75sv8 felis silve
9	182.5	13.2	290	2	Q76LB4	Q76lb4 paralichthy
10	182	13.1	267	2	O02764	O02764 oryctolagus
11	177	12.8	276	2	Q9DDD2	Q9ddd2 gallus gall
12	175	12.6	272	1	TNR4_MOUSE	P47741 mus musculu
13	174.5	12.6	196	2	Q8VCI7	Q8vci7 mus musculu
14	170.5	12.3	211	2	Q8R037	Q8r037 mus musculu
15	170	12.3	274	2	Q7YRL5	Q7yrl5 canis famil
16	168.5	12.2	271	1	TNR4_RAT	P15725 rattus norv
17	162	11.7	277	1	TNR4_HUMAN	P43489 homo sapien
18	158.5	11.4	467	2	Q800I0	Q800i0 gallus gall
19	153	11.0	300	1	TR6B_HUMAN	O95407 homo sapien
20	150	10.8	616	1	TR11_HUMAN	Q9y6q6 homo sapien
21	148.5	10.7	278	2	Q8SQ34	Q8sq34 sus scrofa
22	146	10.5	401	2	Q6PI12	Q6pi12 mus musculu
23	144.5	10.4	269	1	TNR5_BOVIN	Q28203 bos taurus
24	144.5	10.4	289	1	TNR5_MOUSE	P27512 mus musculu
25	143.5	10.4	277	2	Q8WMQ2	Q8wmq2 ovis aries
26	143.5	10.4	289	2	Q8K2X6	Q8k2x6 mus musculu
27	142	10.2	401	1	T11B_RAT	O08727 rattus norv
28	142	10.2	483	2	Q800K7	Q800k7 paralichthy
29	141.5	10.2	169	2	Q9JKE0	Q9jke0 rattus norv
30	141	10.2	401	1	T11B_MOUSE	O08712 mus musculu
31	139.5	10.1	457	2	Q8IVS6	Q8ivs6 homo sapien
32	138	10.0	401	1	T11B_HUMAN	O00300 homo sapien
33	137.5	9.9	651	2	Q98SM6	Q98sm6 gallus gall
34	137	9.9	361	2	Q9AVB0	Q9avb0 phytolacca
35	135.5	9.8	318	2	Q7T2H3	Q7t2h3 oncorhynchu
36	135.5	9.8	387	2	Q6GLN3	Q6gln3 xenopus lae
37	134.5	9.7	625	1	TR11_MOUSE	O35305 mus musculu
38	134.5	9.7	1801	1	LMB2_RAT	P15800 rattus norv
39	133	9.6	435	1	TNR3_HUMAN	P36941 homo sapien
40	130.5	9.4	415	1	TNR3_MOUSE	P50284 mus musculu
41	129.5	9.3	655	1	TR21_HUMAN	O75509 homo sapien
42	129	9.3	461	1	TR1B_HUMAN	P20333 h tumor nec
43	127.5	9.2	1574	1	EFL3_RAT	O88281 rattus norv
44	127.5	9.2	1799	1	LMB2_MOUSE	Q61292 mus musculu
45	126.5	9.1	1799	2	Q8R0Y0	Q8r0y0 mus musculu

ALIGNMENTS

RESULT 1
TR18_HUMAN
ID TR18_HUMAN STANDARD; PRT; 241 AA.
AC Q9Y5U5; O95851; Q9NYJ9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 18 precursor
DE (Glucocorticoid-induced TNFR-related protein) (Activation-inducible
DE TNFR family receptor) (UNQ319/PRO364).
GN Name=TNFRSF18; Synonyms=AITR, GITR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND INTERACTIONS WITH TRAF1; TRAF2 AND
RP TRAF3.
RC TISSUE=Bone marrow;
RX MEDLINE=99175482; PubMed=10074428; DOI=10.1016/S0960-9822(99)80093-1;
RA Gurney A.L., Marsters S.A., Huang R.M., Pitti R.M., Mark D.T.,
RA Baldwin D.T., Gray A.M., Dowd A.D., Brush A.D., Heldens A.D.,
RA Schow A.D., Goddard A.D., Wood W.I., Baker K.P., Godowski P.J.,
RA Ashkenazi A.;
RT "Identification of a new member of the tumor necrosis factor family
RT and its receptor, a human ortholog of mouse GITR.";
RL Curr. Biol. 9:215-218(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=T-cell;
RX MEDLINE=99156876; PubMed=10037686; DOI=10.1074/jbc.274.10.6056;
RA Kwon B., Yu K.-Y., Ni J., Yu G.-L., Jang I.-K., Kim Y.-J., Xing L.,
RA Liu D., Wang S.-X., Kwon B.S.;
RT "Identification of a novel activation-inducible protein of the tumor
RT necrosis factor receptor superfamily and its ligand.";
RL J. Biol. Chem. 274:6056-6061(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Thymus;
RX MEDLINE=20292073; PubMed=10836847;
RA Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA Brunetti L., Migliorati G., Riccardi C.;
RT "Identification of three novel mRNA splice variants of GITR.";
RL Cell Death Differ. 7:408-410(2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,

```
RA   Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA   Godowski P., Gray A.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
RN   [5]
RP   SEQUENCE OF 26-40.
RX   PubMed=15340161; DOI=10.1110/ps.04682504;
RA   Zhang Z., Henzel W.J.;
RT   "Signal peptide prediction based on analysis of experimentally
RT   verified cleavage sites.";
RL   Protein Sci. 13:2819-2824(2004).
CC   -!- FUNCTION: Receptor for TNFSF18. Seems to be involved in
CC       interactions between activated T lymphocytes and endothelial cells
CC       and in the regulation of T cell receptor-mediated cell death.
CC       Mediated NF-kappa-B activation via the TRAF2/NIK pathway.
CC   -!- SUBUNIT: Binds to TRAF1, TRAF2, and TRAF3, but not TRAF5 and
CC       TRAF6.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).
CC       Secreted (isoform 2).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=Q9Y5U5-1; Sequence=Displayed;
CC       Name=2; Synonyms=GITR-D;
CC         IsoId=Q9Y5U5-2; Sequence=VSP_006508;
CC   -!- TISSUE SPECIFICITY: Expressed in lymph node, peripheral blood
CC       leukocytes and weakly in spleen.
CC   -!- INDUCTION: Up-regulated in peripherical mononuclear cells after
CC       antigen stimulation/lymphocyte activation.
CC   -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF125304; AAD22635.1; -.
DR   EMBL; AF117297; AAD19694.1; -.
DR   EMBL; AF241229; AAF63506.1; -.
DR   EMBL; AY358877; AAQ89236.1; -.
DR   Genew; HGNC:11914; TNFRSF18.
DR   MIM; 603905; -.
DR   GO; GO:0005031; F:tumor necrosis factor receptor activity; TAS.
DR   GO; GO:0006916; P:anti-apoptosis; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR001368; TNFR_c6.
DR   PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
DR   PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
KW   Alternative splicing; Direct protein sequencing; Glycoprotein;
KW   Receptor; Repeat; Signal; Transmembrane.
FT   SIGNAL       1     25
FT   CHAIN       26    241       Tumor necrosis factor receptor
FT                               superfamily member 18.
FT   DOMAIN      26    162       Extracellular (Potential).
FT   TRANSMEM   163    183       Potential.
FT   DOMAIN     184    241       Cytoplasmic (Potential).
FT   REPEAT      34     72       TNFR-Cys 1.
FT   REPEAT      74    112       TNFR-Cys 2.
FT   REPEAT     115    153       TNFR-Cys 3.
FT   DISULFID    34     49       By similarity.
FT   DISULFID    74     86       By similarity.
FT   DISULFID    81     94       By similarity.
FT   DISULFID   115    134       By similarity.
FT   DISULFID   128    153       By similarity.
FT   CARBOHYD   146    146       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC   135    241       TQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAA
FT                               CVLLLTSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDAR
FT                               SCQFPEEERGERSAEEKGRLGDLWV -> CWRCRRRPKTPE
FT                               AASSPRKSGASDRQRRRGGWETCGCEPGRPPGPPTAASPSP
FT                               GAPQAAGALRSALGRALLPWQQKWVQEGGSDQRPGPCSSAA
FT                               AAGPCRRERETQSWPPSSLAGPDGVGS (in isoform
FT                               2).
FT                               /FTId=VSP_006508.
FT   CONFLICT    194    201       SQCMWPRE -> K (in Ref. 2).
SQ   SEQUENCE   241 AA;  26000 MW;  90DC3B4AA7E82CBE CRC64;

  Query Match             100.0%;  Score 1386;  DB 1;  Length 241;
  Best Local Similarity   100.0%;  Pred. No. 9.9e-110;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD 60

Qy         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF 120

Qy        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180

Qy        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240

Qy        241 V 241
              |
Db        241 V 241


RESULT 2
TR18_MOUSE
ID   TR18_MOUSE     STANDARD;      PRT;   228 AA.
AC   O35714; Q9JKR1; Q9JKR2; Q9JKR3;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 18 precursor
DE   (Glucocorticoid-induced TNFR-related protein).
GN   Name=Tnfrsf18; Synonyms=Gitr;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM A).
RC   STRAIN=C3H;
RX   MEDLINE=97322352; PubMed=9177197; DOI=10.1073/pnas.94.12.6216;
RA   Nocentini G., Giunchi L., Ronchetti S., Krausz L.T., Bartoli A.,
RA   Moraca R., Migliorati G., Riccardi C.;
RT   "A new member of the tumor necrosis factor/nerve growth factor
RT   receptor family inhibits T cell receptor-induced apoptosis.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:6216-6221(1997).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM A).
RC   STRAIN=BALB/c;
RX   MEDLINE=20256302; PubMed=10798444; DOI=10.1089/104454900314474;
RA   Nocentini G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A.,
RA   Delfino D., Migliorati G., Riccardi C.;
RT   "Gene structure and chromosomal assignment of mouse GITR, a member of
RT   the tumor necrosis factor/nerve growth factor receptor family.";
RL   DNA Cell Biol. 19:205-217(2000).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORMS B; C AND D).
RC   TISSUE=Thymus;
RX   MEDLINE=20292073; PubMed=10836847;
RA   Nocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
RA   Brunetti L., Migliorati G., Riccardi C.;
RT   "Identification of three novel mRNA splice variants of GITR.";
RL   Cell Death Differ. 7:408-410(2000).
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RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM A).
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
CC   -!- FUNCTION: Receptor for TNFSF18. Seems to be involved in
CC       interactions between activated T lymphocytes and endothelial cells
CC       and in the regulation of T cell receptor-mediated cell death.
CC       Mediated NF-kappa-B activation via the TRAF2/NIK pathway (By
CC       similarity).
CC   -!- SUBUNIT: Binds to TRAF1, TRAF2, and TRAF3, but not TRAF5 and TRAF6
CC       (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms A, B and
CC       C); secreted (isoform D).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Name=A;
CC         IsoId=O35714-1; Sequence=Displayed;
CC       Name=B;
CC         IsoId=O35714-2; Sequence=VSP_006510;
CC       Name=C;
CC         IsoId=O35714-3; Sequence=VSP_006511;
CC       Name=D;
CC         IsoId=O35714-4; Sequence=VSP_006509;
CC   -!- TISSUE SPECIFICITY: Preferentially expressed in activated T
CC       lymphocytes.
CC   -!- INDUCTION: Up-regulated in peripherical mononuclear cells after
CC       antigen stimulation/lymphocyte activation.
CC   -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U82534; AAB81243.1; -.
DR   EMBL; AF109216; AAF14231.1; -.
DR   EMBL; AF229432; AAF61566.1; -.
DR   EMBL; AF229433; AAF61567.1; -.
DR   EMBL; AF229434; AAF61568.1; -.
DR   EMBL; AK020762; BAC25639.1; -.
DR   MGD; MGI:894675; Tnfrsf18.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR001368; TNFR_c6.
DR   SMART; SM00181; EGF; 1.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
DR   PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
KW   Alternative splicing; Glycoprotein; Receptor; Repeat; Signal;
KW   Transmembrane.
FT   SIGNAL       1     19       Potential.
FT   CHAIN       20    228       Tumor necrosis factor receptor
FT                               superfamily member 18.
FT   DOMAIN      20    153       Extracellular (Potential).
FT   TRANSMEM   154    174       Potential.
FT   DOMAIN     175    228       Cytoplasmic (Potential).
FT   REPEAT      28     61       TNFR-Cys 1.
FT   REPEAT      62    101       TNFR-Cys 2.
FT   REPEAT     102    142       TNFR-Cys 3.
FT   DISULFID    29     44       By similarity.
FT   DISULFID    62     74       By similarity.
FT   DISULFID    69     82       By similarity.
FT   DISULFID   103    122       By similarity.
FT   DISULFID   116    141       By similarity.
FT   CARBOHYD    36     36       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    40     40       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   121    121       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   134    134       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC   121    228       NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVM
FT                               AACIFFLTTVQLGLHIWQLRRQHMCPRETQPFAEVQLSAED
FT                               ACSFQFPEEERGEQTEEKCHLGGRWP -> KDPAIRGGAVV
FT                               S (in isoform D).
FT                               /FTId=VSP_006509.
FT   VARSPLIC   189    228       ETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP
FT                               -> VLLQRPSHSRRCSCQLRMLAASSSLRRNAGSRQKKSVI
FT                               WGVGGHEAWSSSVPQARRYKTCPAIPLVRAGAMLCTLPWAW
FT                               PCSPQQWRKWVYESGELRLGPMAAFLI (in isoform
FT                               B).
FT                               /FTId=VSP_006510.
FT   VARSPLIC   189    228       ETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP
FT                               -> GQLCPREGENVSQAPHLPQFYYRDPAIRGGAVVS (in
FT                               isoform C).
FT                               /FTId=VSP_006511.
SQ   SEQUENCE   228 AA;  25334 MW;  50D8C275D9C56259 CRC64;
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Query Match 53.1%; Score 735.5; DB 1; Length 228;
Best Local Similarity 57.0%; Pred. No. 1.6e-54;
Matches 134; Conservative 31; Mismatches 61; Indels 9; Gaps 3;

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Qy          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65
              |||:  | |:::|| | |||       ||||||::  |:| : ||| ::        ||:|
Db          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-------PGKE 53

Qy         66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125
                :  |:|| ||:||||| |  |:|:|| ||| |:|||   |||:|: || |||| | :
Db         54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113

Qy        126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQL 185
              |||: ||:|:|||||:||||||||||:|   | |  | |||: | :|||:  ||: ||
Db        114 GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173

Qy        186 GLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
              |||||||| | | |||||   ||  | ||| | |||||||||:: |||  ||  |
Db        174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEKCHLGGRW 227
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RESULT 3
Q8C4K3
ID   Q8C4K3      PRELIMINARY;      PRT;   250 AA.
AC   Q8C4K3;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched
DE   library, clone:C130084C11 product:tumor necrosis factor receptor
```

```
DE   superfamily, member 18, full insert sequence.
GN   Name=Tnfrsf18;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK081878; BAC38357.1; -.
DR   MGD; MGI:894675; Tnfrsf18.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR001368; TNFR_c6.
DR   SMART; SM00181; EGF; 1.
DR   SMART; SM00208; TNFR; 2.
KW   Receptor.
SQ   SEQUENCE   250 AA;  27814 MW;  6963E94F414C16B4 CRC64;

  Query Match             53.1%;  Score 735.5;  DB 2;  Length 250;
  Best Local Similarity   57.0%;  Pred. No. 1.7e-54;
  Matches  134;  Conservative   31;  Mismatches   61;  Indels    9;  Gaps    3;

Qy          7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE 65
              |||:  | |:::|| | |||      ||||||::  |:| : ||| ::        ||:|
Db          1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-------PGKE 53

Qy         66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125
               | :  |:|| ||:|||| |  |:|:|| ||| |:||   |||:|: || |||| | :
Db         54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113

Qy        126 GHCKPWTDCTQFGFLTVPPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQL 185
              |||: ||:|:|||||:||||||||||:|   | |  | |||: | :|||:  ||: ||
Db        114 GHCRLWTNCSQFGFLTMPPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173

Qy        186 GLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
              |||||||| | | |||||   ||  | ||| | |||||||||:: |||  ||  |
Db        174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEKCHLGGRW 227


RESULT 4
Q80WM9
ID   Q80WM9      PRELIMINARY;      PRT;   275 AA.
AC   Q80WM9;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 14 precursor.
GN   Name=Tnfrsf14;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Thymus;
RA   Benencia F., Conejo-Garcia J.R., Courreges M.C., Coukos G.;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY264405; AAO89081.1; -.
DR   HSSP; Q92956; 1JMA.
DR   MGD; MGI:2675303; Tnfrsf14.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR   GO; GO:0006915; P:apoptosis; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR008063; Fas_receptor.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   PRINTS; PR01680; FASRECEPTOR.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
KW   Receptor; Signal.
FT   SIGNAL        1     38       Potential.
SQ   SEQUENCE   275 AA;  30171 MW;  C4A7EAD8EFC0521D CRC64;

  Query Match             14.6%;  Score 202;  DB 2;  Length 275;
  Best Local Similarity   24.6%;  Pred. No. 3.6e-09;
  Matches   65;  Conservative   32;  Mismatches   93;  Indels   74;  Gaps   12;

Qy         22 LSLGQRPTGGPGCGPGRLLLGTGTDARCCRV-----HTTRCCRDYPGEEC---------- 66
              |:| || :  | |     |:|      || :     |  : | :: |  |
Db         30 LNLLQRISAQPSCRQEEFLVGD----ECCPMCNPGYHVKQVCSEHTGTVCAPCPPQTYTA 85

Qy         67 ------------------------CSEWD---CMCVQPEFHC----GDPCCTTCRHHPC 94
                                      || |     | |: | : |     |  | | :| |
Db         86 HANGLSKCLPCGVCDPDMGLLTWQECSSWKDTVCRCI-PGYFCENQDGSHCSTCLQHTTC 144
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Qy          95 PPGQGVQSQGKFSFGFQCIDCASGTFS-GGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 153
               |||| |: :|       | || :|||| || :  | |||:|: |    |  |  : :  |
Db         145 PPGQRVEKRGTHDQDTVCADCLTGTFSLGGTQEECLPWTNCSAFQ-QEVRRGTNSTDTTC 203

Qy         154 VPGSPPAEPLGWLTVVLLAV----AACVLLLTSAQLGLHIWQLRSQCMWPRETQLLLEVP 209
                  :: : ::  :|| :    |      |   :  ||   :  :           || |
Db         204 -----SSQVVYYVVSILLPLVIVGAGIAGFLICTRRHLHTSSVAKE----------LE-P 247

Qy         210 PSTEDARSCQFPEEERGERSAEEK 233
                 :   : :||  | |     ||:
Db         248 FQEQQENTIRFPVTEVGFAETEEE 271


RESULT 5
Q71F55
ID   Q71F55      PRELIMINARY;      PRT;   276 AA.
AC   Q71F55;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Herpes virus entry mediator.
GN   Name=Hvem;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvJ;
RA   Rickert S., Granger S.W., Ko M., Shukla D., Spear P.G., Kronenberg M.,
RA   Ware C.F.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF515707; AAQ08183.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR   GO; GO:0006915; P:apoptosis; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR008063; Fas_receptor.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   PRINTS; PR01680; FASRECEPTOR.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
SQ   SEQUENCE   276 AA;  30327 MW;  4A615FB2629E9125 CRC64;

  Query Match             14.5%;  Score 201.5;  DB 2;  Length 276;
  Best Local Similarity   23.9%;  Pred. No. 4e-09;
  Matches   64;  Conservative   35;  Mismatches   88;  Indels   81;  Gaps   12;

Qy          22 LSLGQRPTGGPGCGPGRLLLGTGTDARCCRV-----HTTRCCRDYPGEEC---------- 66
               |:| || :  | |      |:|      || :     |  : | :: |  |
Db          30 LNLLQRISAQPSCRQEEFLVGD----ECCPMCNPGYHVKQVCSEHTGTVCAPCPPQTYTA 85

Qy          67 -------------------------CSEWD---CMCVQPEFHC----GDPCCTTCRHHPC 94
                                        || |    | |: | : |    |  | | :|  |
Db          86 HANGLSKCLPCGVCDPDMGLLTWQECSSWKDTVCRCI-PGYFCENQDGSHCSTCLQHTTC 144

Qy          95 PPGQGVQSQGKFSFGFQCIDCASGTFS-GGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 153
               |||| |: :|       | || :|||| || :  | |||:|: |    |  |  : :  |
Db         145 PPGQRVEKRGTHDQDTVCADCLTGTFSLGGTQEECLPWTNCSAFQ-QEVRRGTNSTDTTC 203

Qy         154 VPGSPPAEPLGWLTVVLLAVA------ACVLLLTSAQLGLHIWQLRSQCMWPRETQLLLE 207
                  :: : ::  :|| :       |  |: |   |                : :  |
Db         204 -----SSQVVYYVVSILLPLVIVGVGIAGFLICTRRHL-------------HTSSVAKE 244

Qy         208 VPPSTEDAR--SCQFPEEERGERSAEEK 233
               : |  :: :  : :||  | |    ||:
Db         245 LEPFQQEQQENTIRFPVTEVGFAETEEE 272
```

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RESULT 6
TNR9_MOUSE
ID   TNR9_MOUSE     STANDARD;      PRT;   256 AA.
AC   P20334;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB
DE   ligand receptor) (T-cell antigen 4-1BB) (CD137 antigen).
GN   Name=Tnfrsf9; Synonyms=Cd137, Cd157, ILA, Ly63;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89184547; PubMed=2784565;
RA   Kwon B.S., Weissman S.M.;
RT   "cDNA sequences of two inducible T-cell genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   MEDLINE=94179805; PubMed=8133039;
RA   Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.;
RT   "Genomic organization and chromosomal localization of the T-cell
RT   antigen 4-1BB.";
RL   J. Immunol. 152:2256-2262(1994).
RN   [3]
RP   CHARACTERIZATION, AND SEQUENCE OF 24-29.
RX   MEDLINE=93139510; PubMed=7678621;
RA   Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kin K.K., Pickard R.T.,
RA   Kwon B.S.;
RT   "Inducible T cell antigen 4-1BB. Analysis of expression and
RT   function.";
RL   J. Immunol. 150:771-781(1993).
CC   -!- FUNCTION: Receptor for TNFSF14/4-1BBL. Possibly active during T
CC       cell activation.
CC   -!- SUBUNIT: Principally an homodimer, but also found as a monomer.
CC       Associates with p56-LCK. Interacts with TRAF1, TRAF2 and TRAF3 (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed on the surface of activated T cells.
CC   -!- INDUCTION: Optimal by PMA and ionomycin.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J04492; AAA40167.1; -.
DR   EMBL; U02567; AAA93113.1; -.
DR   PIR; B32393; B32393.
DR   PDB; 1D0J; X-ray; G/H/I/J/K=230-236.
DR   MGD; MGI:1101059; Tnfrsf9.
DR   InterPro; IPR009030; Grow_fac_recept.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
KW   3D-structure; Direct protein sequencing; Glycoprotein; Receptor;
KW   Repeat; Signal; Transmembrane.
FT   SIGNAL        1     23
FT   CHAIN        24    256       Tumor necrosis factor receptor
FT                                 superfamily member 9.
FT   DOMAIN       24    187       Extracellular (Potential).
FT   TRANSMEM    188    208       Potential.
FT   DOMAIN      209    256       Cytoplasmic (Potential).
```

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FT   REPEAT       24     45       TNFR-Cys 1.
FT   REPEAT       46     85       TNFR-Cys 2.
FT   REPEAT       86    117       TNFR-Cys 3.
FT   REPEAT      118    159       TNFR-Cys 4.
FT   DISULFID     28     37       By similarity.
FT   DISULFID     31     44       By similarity.
FT   DISULFID     47     61       By similarity.
FT   DISULFID     64     77       By similarity.
FT   DISULFID     67     85       By similarity.
FT   DISULFID     87     93       By similarity.
FT   DISULFID     98    105       By similarity.
FT   DISULFID    101    116       By similarity.
FT   DISULFID    119    133       By similarity.
FT   DISULFID    139    158       By similarity.
FT   CARBOHYD    128    128       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    138    138       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   256 AA;  27598 MW;  93A10D03C60813C4 CRC64;

  Query Match             14.2%;  Score 197;  DB 1;  Length 256;
  Best Local Similarity   28.8%;  Pred. No. 9e-09;
  Matches   64;  Conservative   25;  Mismatches   85;  Indels   48;  Gaps   10;

Qy         34 CGPGRL-LLGTGTDARCCRVHTTRCCRDYPGEECCSEW---DCMCVQPEFHCGDPCCTTC 89
              | |     :|   :   |||    |   :  :: ||     :| |::  |||  | || |
Db         47 CPPSTFSSIGGQPNCNICRV----CAGYFRFKKFCSSTHNAECECIE-GFHCLGPQCTRC 101

Qy         90 RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGH-EGHCKPWTDCTQFGFLTVFPGNKT 148
                | ||| :  ||       |  |: |||:  :  | |:|||:|:  |   :  |
Db        102 -EKDCRPGQELTKQG-------CKTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTE 153

Qy        149 HNAVCVP---------------GSPPAEPLGWLTVVLLAVAACVLLLTSAQLGLHIWQL 192
               : || |               | |    |  ||: |   :| :| |      : |  |
Db        154 KDVVCGPPVVSFSPSTTISVTPEGGPGGHSLQVLTLFLALTSALLLAL------IFITLL 207

Qy        193 RSQCMWPRETQLLLEVPP--------STEDARSCQFPEEERG 226
              |   | |:   :   |          ||| ||: |:|| |
Db        208 FSVLKWIRKKFPHIFKQPFKKTTGAAQEEDACSCRCPQEEEG 249


RESULT 7
TNR9_HUMAN
ID   TNR9_HUMAN     STANDARD;      PRT;   255 AA.
AC   Q07011;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   25-JAN-2005 (Rel. 46, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB
DE   ligand receptor) (T-cell antigen 4-1BB homolog) (T-cell antigen ILA)
DE   (CD137 antigen).
GN   Name=TNFRSF9; Synonyms=CD137, ILA;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=94374434; PubMed=8088337;
RA   Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J.,
RA   Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G.;
RT   "Molecular and biological characterization of human 4-1BB and its
RT   ligand.";
RL   Eur. J. Immunol. 24:2219-2227(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=94085794; PubMed=8262389; DOI=10.1016/0378-1119(93)90110-O;
RA   Schwarz H., Tuckwell J., Lotz M.;
RT   "A receptor induced by lymphocyte activation (ILA): a new member of
RT   the human nerve-growth-factor/tumor-necrosis-factor receptor family.";
RL   Gene 134:295-298(1993).
RN   [3]
RP   REVISION TO 107.
RA   Schwarz H.;
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=95347766; PubMed=7622190; DOI=10.1016/0165-2478(94)00227-I;
RA   Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E.,
RA   Kwon B.S.;
RT   "Characterization of human homologue of 4-1BB and its ligand.";
RL   Immunol. Lett. 45:67-73(1995).
RN   [5]
RP   SEQUENCE FROM N.A., AND VARIANTS THR-56; ASN-115 AND ASP-176.
RA   Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,
RA   Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA   Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RT   "NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department
RT   of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL   Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   SEQUENCE FROM N.A.
RA   Pearce A.;
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [8]
RP   SEQUENCE OF 24-38.
RX   PubMed=15340161; DOI=10.1110/ps.04682504;
RA   Zhang Z., Henzel W.J.;
RT   "Signal peptide prediction based on analysis of experimentally
RT   verified cleavage sites.";
RL   Protein Sci. 13:2819-2824(2004).
RN   [9]
RP   INTERACTIONS WITH TRAF1; TRAF2 AND TRAF3.
RX   MEDLINE=98078711; PubMed=9418902;
RA   Arch R.H., Thompson C.B.;
RT   "4-1BB and Ox40 are members of a tumor necrosis factor (TNF)-nerve
RT   growth factor receptor subfamily that bind TNF receptor-associated
RT   factors and activate nuclear factor kappaB.";
RL   Mol. Cell. Biol. 18:558-565(1998).
RN   [10]
RP   INTERACTIONS WITH TRAF1 AND TRAF2.
RX   MEDLINE=98270914; PubMed=9607925;
RA   Saoulli K., Lee S.Y., Cannons J.L., Yeh W.C., Santana A.,
RA   Goldstein M.D., Bangia N., DeBenedette M.A., Mak T.W., Choi Y.,
RA   Watts T.H.;
RT   "CD28-independent, TRAF2-dependent costimulation of resting T cells by
RT   4-1BB ligand.";
RL   J. Exp. Med. 187:1849-1862(1998).
RN   [11]
RP   INTERACTION WITH LRR-REPEAT PROTEIN 1/LRR-1.
RX   MEDLINE=21662677; PubMed=11804328;
```

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RA   Jang I.-K., Lee Z.-H., Kim H.-H., Hill J.M., Kim J.-D., Kwon B.S.;
RT   "A novel leucine-rich repeat protein (LRR-1): potential involvement in
RT   4-1BB-mediated signal transduction.";
RL   Mol. Cells 12:304-312(2001).
CC   -!- FUNCTION: Receptor for TNFSF14/4-1BBL. Possibly active during T
CC       cell activation.
CC   -!- SUBUNIT: Interacts with TRAF1, TRAF2 and TRAF3. Interacts with
CC       LRR-repeat protein 1/LRR-1.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed on the surface of activated T cells.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CDw137 entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdw137.htm".
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U03397; AAA53133.1; -.
DR   EMBL; L12964; AAA62478.2; -.
DR   EMBL; AY438976; AAR05440.1; -.
DR   EMBL; AL009183; CAB57398.1; -.
DR   EMBL; BC006196; AAH06196.1; -.
DR   PIR; I38426; I38426.
DR   HSSP; Q92956; 1JMA.
DR   Genew; HGNC:11924; TNFRSF9.
DR   H-InvDB; HIX0000096; -.
DR   MIM; 602250; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0004872; F:receptor activity; TAS.
DR   GO; GO:0006917; P:induction of apoptosis; TAS.
DR   GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Direct protein sequencing; Glycoprotein; Polymorphism; Receptor;
KW   Repeat; Signal; Transmembrane.
FT   SIGNAL        1     23
FT   CHAIN        24    255       Tumor necrosis factor receptor
FT                                 superfamily member 9.
FT   DOMAIN       24    186       Extracellular (Potential).
FT   TRANSMEM    187    213       Potential.
FT   DOMAIN      214    255       Cytoplasmic (Potential).
FT   REPEAT       24     45       TNFR-Cys 1.
FT   REPEAT       47     86       TNFR-Cys 2.
FT   REPEAT       87    118       TNFR-Cys 3.
FT   REPEAT      119    159       TNFR-Cys 4.
FT   DOMAIN      214    255       Interaction with LRR-1.
FT   DISULFID     28     37       By similarity.
FT   DISULFID     31     45       By similarity.
FT   DISULFID     48     62       By similarity.
FT   DISULFID     65     78       By similarity.
FT   DISULFID     68     86       By similarity.
FT   DISULFID     88     94       By similarity.
FT   DISULFID     99    106       By similarity.
FT   DISULFID    102    117       By similarity.
FT   DISULFID    121    133       By similarity.
FT   DISULFID    139    158       By similarity.
FT   CARBOHYD    138    138       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    149    149       N-linked (GlcNAc. . .) (Potential).
FT   VARIANT      56     56       A -> T.
FT                                 /FTId=VAR_018920.
FT   VARIANT     115    115       K -> N.
FT                                 /FTId=VAR_018921.
FT   VARIANT     176    176       A -> D.
FT                                 /FTId=VAR_018922.
SQ   SEQUENCE   255 AA;  27899 MW;  F3A563FE5EF00460 CRC64;
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  Query Match           14.1%;  Score 195.5;  DB 1;  Length 255;
  Best Local Similarity   28.8%;  Pred. No. 1.2e-08;
  Matches   66;  Conservative   21;  Mismatches   81;  Indels   61;  Gaps   12;

Qy         34 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG-----EECCS----EWDCMCVQPEFHCGDP 84
              | |          |   | | :      ||    |      :|| |     | ||    | |||
Db         48 CPPNSFSSAGG--QRTCDI-----CRQCKGVFRTRKECSSTSNAECDC---TPGFHCLGA 97

Qy         85 CCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFP 144
              |: |    |  || :  :|       | ||  |||:    | |:|||:|:  |   :
Db         98 GCSMC-EQDCKQGQELTKKG-------CKDCCFGTFNDQKRGICRPWTNCSLDGKSVLVN 149

Qy        145 GNKTHNAVCVPG-----------SPPA---EPLGWLTVV--LLAVAACVLLLTSAQLGLH 188
              | |  : || |            :|||   ||     ::   ||: :  ||     | |
Db        150 GTKERDVVCGPSPADLSPGASSVTPPAPAREPGHSPQIISFFLALTSTALLFLLFFLTLR 209

Qy        189 -----------IWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERG 226
                        ::  :   | | :|          ||  ||:||||| |
Db        210 FSVVKRGRKKLLYIFKQPFMRPVQT-------TQEEDGCSCRFPEEEEG 251


RESULT 8
Q75SV8
ID   Q75SV8      PRELIMINARY;      PRT;   270 AA.
AC   Q75SV8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   CD134 homologue.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Shimojima M., Miyazawa T., Ikeda Y., McMonagle E.L., Haining H.,
RA   Akashi H., Takeuchi Y., Hosie M.J., Willett B.J.;
RT   "Use of CD134 as a primary receptor by the feline immunodeficiency
RT   virus.";
RL   Science 0:0-0(2004).
DR   EMBL; AB128982; BAD11363.1; -.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ   SEQUENCE   270 AA;  28731 MW;  36A40BAD261140D1 CRC64;

  Query Match           13.8%;  Score 191;  DB 2;  Length 270;
  Best Local Similarity   27.3%;  Pred. No. 3e-08;
  Matches   65;  Conservative   20;  Mismatches   73;  Indels   80;  Gaps   12;

Qy         39 LLLGTGTDARCCRVHTT-----RCCRDYP---GEE--CCSEWDCMCVQPEFHCG------ 82
              |:|||      |  |  |     :|| : |   | |  |  : |  |:|    |
Db         22 LVLGTAAALHC--VGNTYPKDGKCCSECPPGYGMESRCSGDQDTKCLQ----CASGFYNE 75

Qy         83 ----DPC--CTTCRHHP-------CPPGQ--------GVQSQGKFSFGFQCIDCASGTFS 121
                  :||  || |             | | |       | : |  :  |  |  |  | ||
Db         76 AVNYEPCKPCTQCNQRSGSEPKQRCTPTQDTVCRCRPGTEPQDGYDRGVDCAPCPPGHFS 135

Qy        122 GGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLT 181
               | :  |||||:||  |  |: | ::  :|||   ||||
Db        136 PGDDQACKPWTNCTLAGKRTLRPASQGSDAVCEDRSPPATT------------------- 176

Qy        182 SAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFP-----EEERGERSAEEKG 234
                    |: :   : |  ||       |:|   |: | |      |  || : |   |
Db        177 -------PWETQGPPVRPPTTQ------PTTAWPRTSQEPFTPPAEPPRGPQLAAVLG 221


RESULT 9
Q76LB4
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ID   Q76LB4      PRELIMINARY;      PRT;   290 AA.
AC   Q76LB4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   CD40.
GN   Name=CD40;
OS   Paralichthys olivaceus (Japanese flounder).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC   Pleuronectoidei; Paralichthyidae; Paralichthys.
OX   NCBI_TaxID=8255;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Park C., Hirono I., Aoki T.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Park C., Hirono I., Aoki T.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB081752; BAC87848.1; -.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR001368; TNFR_c6.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
SQ   SEQUENCE   290 AA;  32396 MW;  B6FCF9E35305DFAA CRC64;

  Query Match             13.2%;  Score 182.5;  DB 2;  Length 290;
  Best Local Similarity   25.8%;  Pred. No. 1.7e-07;
  Matches   63;  Conservative   24;  Mismatches  108;  Indels   49;  Gaps   11;

Qy         34 CGPG--RLLLGTGTDARCCRVHTTRCCRDYPGEECC--------------------SEW 70
              ||||  |:   | || :|           |  | |                      :
Db         40 CGPGTRRMSQSTCTDPQCAECGNREYQDRYTREAQCKRQPYCDPNKNLRVTKPESKTKQS 99

Qy         71 DCMCVQPEFHCGDPCCTTC-RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGH--EGH 127
               |:|:   |||    | ||  |  | |||  : :|  :    |  |  |:|| |
Db        100 PCICLL-GFHCSSGTCVTCVPHATCKPGQWAKIKGNLTHDTVCESCPEGSFSTSHSWSSV 158

Qy        128 CKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVL----LAVAACVLLLTSA 183
              |  ||:| : |:      |    : :||   ||    | :  |:    |||   :: |
Db        159 CTKWTEC-ESGYHIQESGTNESDNICV--EPPRHHGGLIACVVAVGSLAVVGLMVCLCKG 215

Qy        184 QLGLHIWQLRSQCMWPRETQLLLEVPPS---------TEDARSCQFPEEER---GERSAE 231
              :          |   :|    |: ||          ||:     | |||     |::
Db        216 ETKQRAKDYLESCHGDKEN---LQREPSLVLFTTLDETENHELLPFTEEEEMKIPEKTTR 272

Qy        232 EKGR 235
               |||
Db        273 TKGR 276


RESULT 10
O02764
ID   O02764      PRELIMINARY;      PRT;   267 AA.
AC   O02764;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   OX40 precursor (Fragment).
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Chbb:HM;
RA   Isono T., Seto A.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB003911; BAA20059.1; -.
DR   HSSP; Q92956; 1JMA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Signal.
FT   NON_TER       1      1
FT   SIGNAL       <1     18       Potential.
FT   CHAIN        19    267       OX40.
SQ   SEQUENCE   267 AA;  28489 MW;  A8B4CD3173C9500B CRC64;

  Query Match             13.1%;  Score 182;  DB 2;  Length 267;
  Best Local Similarity   27.8%;  Pred. No. 1.7e-07;
  Matches   68;  Conservative   15;  Mismatches   88;  Indels   74;  Gaps   12;

Qy         12 ALCGLA-LLCALSLGQRPTGGPGC------GPGRLLL----GTGTDARCCRVHTTRCCRD 60
              |  ||| ||  | ||  |   | |      |  |  |    | |  :|| |   | |
Db          4 AALGLALLLLGLLLGAEPR--PDCVGDTYPGGDRCCLECQPGYGMVSRCNRSQDTICHPC 61

Qy         61 YPG--EECCSEWDCM-CVQ--------PEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFG 109
               ||   |  :   |  | |        |:  |     | ||   | |  | ||   :  |
Db         62 EPGFYNEAVNYQACKPCTQCNRRSGSEPQQECTHTRDTVCR---CRP--GTQPLNGYKHG 116

Qy        110 FQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC-----------VPGS 157
                |  |  | || |:   |:|||:||  |  |: | :   :|||          | :
Db        117 VDCAPCPQGHFSEGNNRACRPWTNCTLAGKRTLQPASSISDAVCEDRSSLATQPWETPSA 176

Qy        158 PPAEPLGWLTVVLLAVAACVLLLTSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARS 217
              |   |                                |:   |||  |       |||    :
Db        177 PYRPPTA---------------------------RTSTAWPRTAQ-----GPSTPTLEA 203

Qy        218 CQFPE 222
               : |:
Db        204 SKGPQ 208


RESULT 11
Q9DDD2
ID   Q9DDD2      PRELIMINARY;      PRT;   276 AA.
AC   Q9DDD2;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   CD40-homologue.
GN   Name=TNFSF5;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Tregaskes C.A.;
RL   Thesis (2001), University of Reading, Reading, UNITED KINGDOM.
DR   EMBL; AJ293700; CAC20218.1; -.
DR   HSSP; Q92956; 1JMA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR   GO; GO:0006915; P:apoptosis; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR008063; Fas_receptor.
DR   InterPro; IPR001005; Myb_DNA_binding.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   PRINTS; PR01680; FASRECEPTOR.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00037; MYB_1; UNKNOWN_1.
DR   PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
SQ   SEQUENCE   276 AA;  30009 MW;  4040B7E0DB82454E CRC64;
```

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  Query Match             12.8%;  Score 177;  DB 2;  Length 276;
  Best Local Similarity   24.8%;  Pred. No. 4.8e-07;
  Matches   73;  Conservative   23;  Mismatches   90;  Indels  108;  Gaps   16;

Qy         16 LALLCALSLGQRPTGGPGCG-PGRLLLGTGTDARCCR----VHTTRCC-RDYPGEECCSE 69
              | ||||| |         ||| ||         ||  |       |  ||| |  ||::  ||
Db          7 LGLLCALLL--------GCGQPG--------DAVNCSDKQYEHKGRCCNRCQPGKKLASE 50

Qy         70 --------------------WD-----------------------------CMCVQPEF 79
                                   |                             | | :
Db         51 CNDTEDSVCTPCENGQYQHSWTKERHCTPHEICEDNAGLIVKRHGNATHNTVCQC-RAGM 109

Qy         80 HCGDPCCTTC-RHHPCPPGQG-VQSQGKFSFGFQCIDCASGTFS--GGHEGHCKPWTDCT 135
              || |  | ||  : ||  | | | :  :       |  || ||||       |  || |
Db        110 HCSDASCQTCVENEPCKQGFGFVAAMAEARMTSPCEPCAEGTFSNVSSKTEPCHFWTSCE 169

Qy        136 QFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQLGLHIWQL--- 192
              : | :    |  | : :|   |      |  |  :  ||  |:       :|: |: |
Db        170 EKGLVVKVKGTNTSDVIC--ESSRRSSLSVLIPITAAVVTCL-------VGICIYCLVHT 220

Qy        193 --------RSQCMWPRETQLLLEVPPSTEDARSCQFPEEER---GERSAEEKGR 235
                     :::   |||          |:      || :|    |:  |:| |:
Db        221 DLRRRGPKQAEAEAPREL--------VTQQPEEVDFPVQETLLGGQPVAQEDGK 266
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```
RESULT 12
TNR4_MOUSE
ID   TNR4_MOUSE     STANDARD;      PRT;   272 AA.
AC   P47741;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Tumor necrosis factor receptor superfamily member 4 precursor (OX40L
DE   receptor) (OX40 antigen).
GN   Name=Tnfrsf4; Synonyms=OX40, Txgp1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   MEDLINE=94044750; PubMed=8228223;
RA   Calderhead D.M., Buhlmann J.E., van den Eertwegh A.J., Claassen E.,
RA   Noelle R.J., Fell H.;
RT   "Cloning of mouse Ox40: a T cell activation marker that may mediate T-
RT   B cell interactions.";
RL   J. Immunol. 151:5261-5271(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95255413; PubMed=7737295;
RA   Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA   Barclay A.N.;
RT   "Gene structure and chromosomal localization of the mouse homologue of
RT   rat OX40 protein.";
RL   Eur. J. Immunol. 25:926-930(1995).
CC   -!- FUNCTION: Receptor for TNFSF4/OX40L/GP34.
CC   -!- SUBUNIT: Interacts with TRAF2, TRAF3 and TRAF5 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z21674; CAA79772.1; -.
DR   EMBL; X85214; CAA59476.1; -.
DR   PIR; I48700; I48700.
DR   HSSP; Q92956; 1JMA.
DR   MGD; MGI:104512; Tnfrsf4.
DR   GO; GO:0005886; C:plasma membrane; IDA.
DR   GO; GO:0006968; P:cellular defense response; IMP.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 3.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS00652; TNFR_NGFR_1; 2.
DR   PROSITE; PS50050; TNFR_NGFR_2; 2.
KW   Antigen; Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
FT   SIGNAL        1     19       Potential.
FT   CHAIN        20    272       Tumor necrosis factor receptor
FT                                superfamily member 4.
FT   DOMAIN       20    211       Extracellular (Potential).
FT   TRANSMEM    212    236       Potential.
FT   DOMAIN      237    272       Cytoplasmic (Potential).
FT   REPEAT       26     61       TNFR-Cys 1.
FT   REPEAT       62    103       TNFR-Cys 2.
FT   REPEAT      104    124       TNFR-Cys 3 (incomplete).
FT   REPEAT      125    165       TNFR-Cys 4.
FT   DISULFID     27     38       By similarity.
FT   DISULFID     39     52       By similarity.
FT   DISULFID     42     60       By similarity.
FT   DISULFID     63     77       By similarity.
FT   DISULFID     80     95       By similarity.
FT   DISULFID     83    103       By similarity.
FT   DISULFID    105    123       By similarity.
FT   DISULFID    126    139       By similarity.
FT   DISULFID    145    164       By similarity.
FT   CARBOHYD    144    144       N-linked (GlcNAc. . .) (Potential).
FT   CONFLICT     15     15       A -> G (in Ref. 2).
SQ   SEQUENCE   272 AA;  30153 MW;  06E7BB4156F0D08E CRC64;
```

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  Query Match             12.6%;  Score 175;  DB 1;  Length 272;
  Best Local Similarity   26.7%;  Pred. No. 7e-07;
  Matches   58;  Conservative   19;  Mismatches   70;  Indels   70;  Gaps   10;

Qy         39 LLLGTGTDAR--CCRVHT----TRCCRD-YPG----EECCSEWDCMCVQPEFHCGDPC-- 85
              | |  |  ||   |  ||     :|||: ||      |    | :|         ||
Db         14 LALTLGVTARRLNCVKHTYPSGHKCCRECQPGHGMVSRCDHTRDTLC--------HPCET 65

Qy         86 --------------CTTCRHHP-----------------CPPGQGVQSQGKFSFGFQCID 114
                           || | |                  | ||   :    :  |  |:
Db         66 GFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTQDTVCRCRPGTQPRQDSGYKLGVDCVP 125

Qy        115 CASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVA 174
              |  | || |:   |||||:||  |  |  | : : :|||   |            |||
Db        126 CPPGHFSPGNNQACKPWTNCTLSGKQTRHPASDSLDAVCEDRS-----------LLA-- 171

Qy        175 ACVLLLTSAQLGLHIWQLRSQCMWPRETQLLLEVPPS 211
                ||  : :      ::|  :||| ::  |  ||:
Db        172 --TLLWETQRPTFRPTTVQSTTVWPRTSE--LPSPPT 204
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RESULT 13
Q8VC17
ID   Q8VC17      PRELIMINARY;      PRT;   196 AA.
AC   Q8VC17;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Tnfrsf14 protein (Fragment).
GN   Name=Tnfrsf14;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Liver;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Liver;
RA   Strausberg R.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC022125; AAH22125.1; -.
DR   HSSP; Q92956; 1JMA.
DR   MGD; MGI:2675303; Tnfrsf14.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR   GO; GO:0006915; P:apoptosis; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   Pfam; PF00020; TNFR_c6; 2.
DR   PRINTS; PR01680; FASRECEPTOR.
DR   SMART; SM00208; TNFR; 3.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   196 AA;  21555 MW;  2AB3FF8905E260E8 CRC64;

  Query Match             12.6%;  Score 174.5;  DB 2;  Length 196;
  Best Local Similarity   27.3%;  Pred. No. 5.7e-07;
  Matches   50;  Conservative   28;  Mismatches   68;  Indels   37;  Gaps    9;

Qy         67 CSEWD---CMCVQPEFHC----GDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGT 119
              || |    | |: | : |    |  | |  :|  ||||| |: :|       | || :||
Db         31 CSSWKDTVCRCI-PGYFCENQDGSHCSTCLQHTTCPPGQRVEKRGTHDQDTVCADCLTGT 89

Qy        120 FS-GGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVA---- 174
              || || :  | |||:|: |    |  |  : :  |      :: : ::  :|| :
Db         90 FSLGGTQEECLPWTNCSAFQ-QEVRRGTNSTDTTC-----SSQVVYYVVSILLPLVIVGV 143

Qy        175 --ACVLLLTSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDAR--SCQFPEEERGERSA 230
                 |  |: |   |                  : :  |: |  :: :  : :||  | |
Db        144 GIAGFLICTRRHL--------------HTSSVAKELEPFQQEQQENTIRFPVTEVGFAET 189

Qy        231 EEK 233
              |||:
Db        190 EEE 192


RESULT 14
Q8R037
ID   Q8R037      PRELIMINARY;      PRT;   211 AA.
AC   Q8R037;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Tnfrsf9 protein.
GN   Name=Tnfrsf9;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Uterus;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Uterus;
RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC028507; AAH28507.1; -.
DR   HSSP; Q92956; 1JMA.
DR   MGD; MGI:1101059; Tnfrsf9.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   InterPro; IPR011061; Antihaemostatic.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 2.
DR   PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
SQ   SEQUENCE   211 AA;  22452 MW;  1EECA84EA32A8D50 CRC64;

  Query Match             12.3%;  Score 170.5;  DB 2;  Length 211;
  Best Local Similarity   27.3%;  Pred. No. 1.3e-06;
  Matches   54;  Conservative   22;  Mismatches   77;  Indels   45;  Gaps    8;

Qy         34 CGPGRL-LLGTGTDARCCRVHTTRCCRDYPGEECCSEW---DCMCVQPEFHCGDPCCTTC 89
              | |     :|   :   |||    |   :  :: ||     :| |::  |||  | || |
Db         47 CPPSTFSSIGGQPNCNICRV----CAGYFRFKKFCSSTHNAECECIE-GFHCLGPQCTRC 101

Qy         90 RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGH-EGHCKPWTDCTQFGFLTVFPGNKT 148
                 | ||| :  ||        |  |: |||:  :  | |:|||:|:  |   :  |
Db        102 -EKDCRPGQELTKQG-------CKTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTE 153

Qy        149 HNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQLGLHIWQLRSQCMWPRETQLLLEV 208
              : || |      |   ::|      |       :||
Db        154 KDVVCGPPVVSFSPSTTISVTPEGGPAFKKTTGAAQ---------------------- 189

Qy        209 PPSTEDARSCQFPEEERG 226
                 ||| ||: |:|| |
Db        190 ---EEDACSCRCPQEEEG 204


RESULT 15
Q7YRL5
ID   Q7YRL5      PRELIMINARY;      PRT;   274 AA.
AC   Q7YRL5;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   CD40.
GN   Name=CD40;
OS   Canis familiaris (Dog).
```

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yang S., Sim G.-K.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY333789; AAP86653.1; -.
DR   HSSP; P25942; 1FLL.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00020; TNFR_c6; 1.
DR   SMART; SM00208; TNFR; 4.
DR   PROSITE; PS00652; TNFR_NGFR_1; 1.
DR   PROSITE; PS50050; TNFR_NGFR_2; 3.
SQ   SEQUENCE   274 AA;  30284 MW;  9723789A07FAB6DB CRC64;

  Query Match             12.3%;  Score 170;  DB 2;  Length 274;
  Best Local Similarity   26.1%;  Pred. No. 1.9e-06;
  Matches   61;  Conservative   20;  Mismatches  107;  Indels   46;  Gaps    8;

Qy         34 CGPGRLLLGTGTDARCCRVHTTRCCRDYPGE---------------------------EC 66
              | ||  |:       |      | | |   ||                           |
Db         41 CPPGEKLVND-----CLHTIDTECTRCQTGEFLDTWNAERHCHQHKYCDPNLGLHVEKEG 95

Qy         67 CSEWDCMCVQPE-FHCGDPCCTTCRHHP-CPPGQGVQSQGKFSFGFQCIDCASGTFSGGH 124
               || |  |   |  || :  | :|  |  |||| ||:          |  |  | ||
Db         96 TSETDTTCTCDEGLHCTNAACESCTMHSLCPPGLGVKQIATGISDTICDPCPIGFFSNVS 155

Qy        125 EG--HCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTS 182
              | ||| |   | : |  |    : :| |  |    |  : | ::     |:|| |
Db        156 SALEKCHPWTSCETKGLVKVQAGTNKTDVICGP-QPRLRAL--VVVPIIMGILLVVLLVS 212

Qy        183 AQLGLHIWQLRSQCMWPRETQLLLEVP-------PSTEDARSCQFPEEEERGERS 229
              | :   : :  :: |:    : | | |       |  |    ||   :| |: |
Db        213 ACIRKVVKKPENKVMYQDPVEDLEEFPMPPHSIAPVQETLHGCQPVTQEDGKES 266


Search completed: October 26, 2005, 15:51:39
Job time : 119.701 secs
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